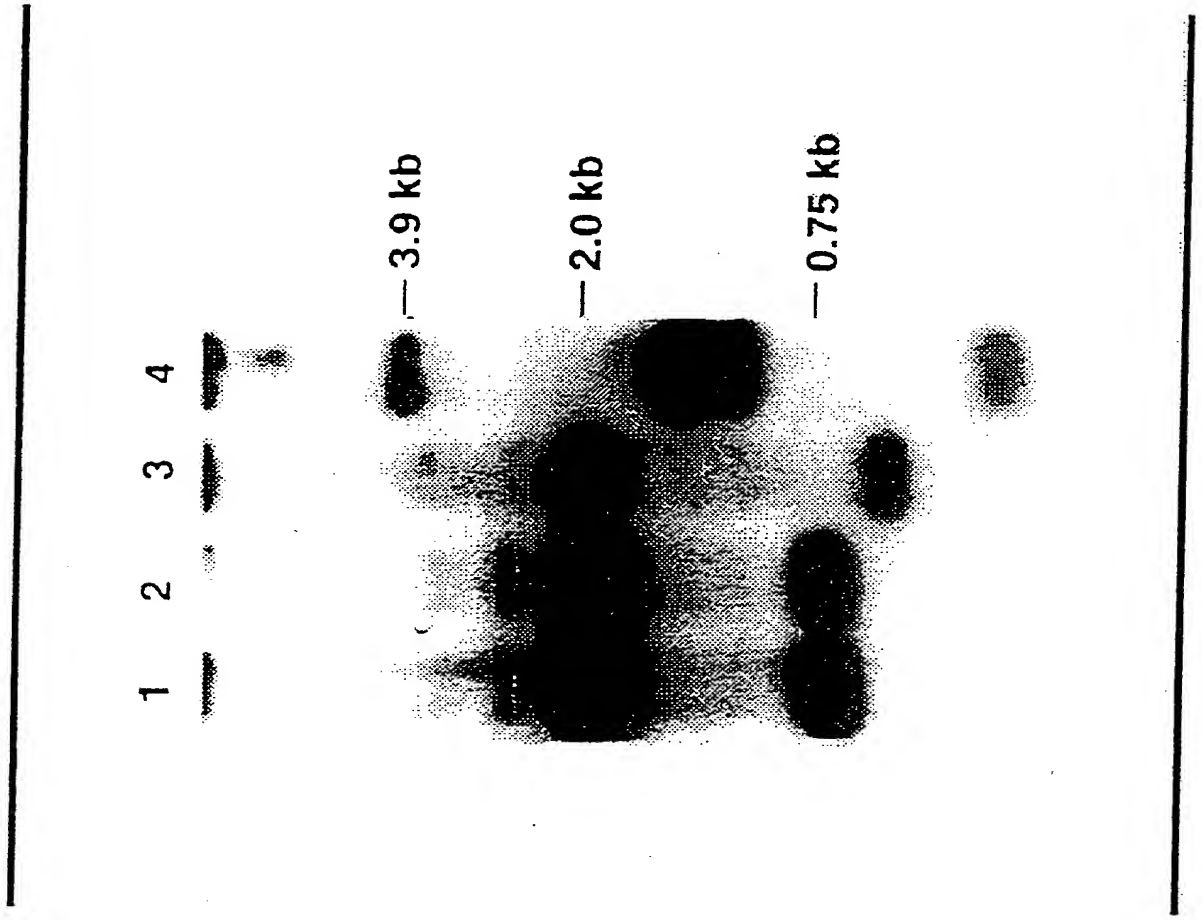


FIGURE 1

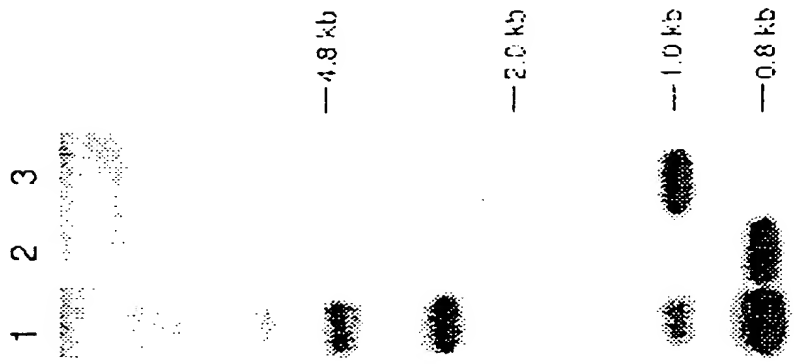


FIGURE 2

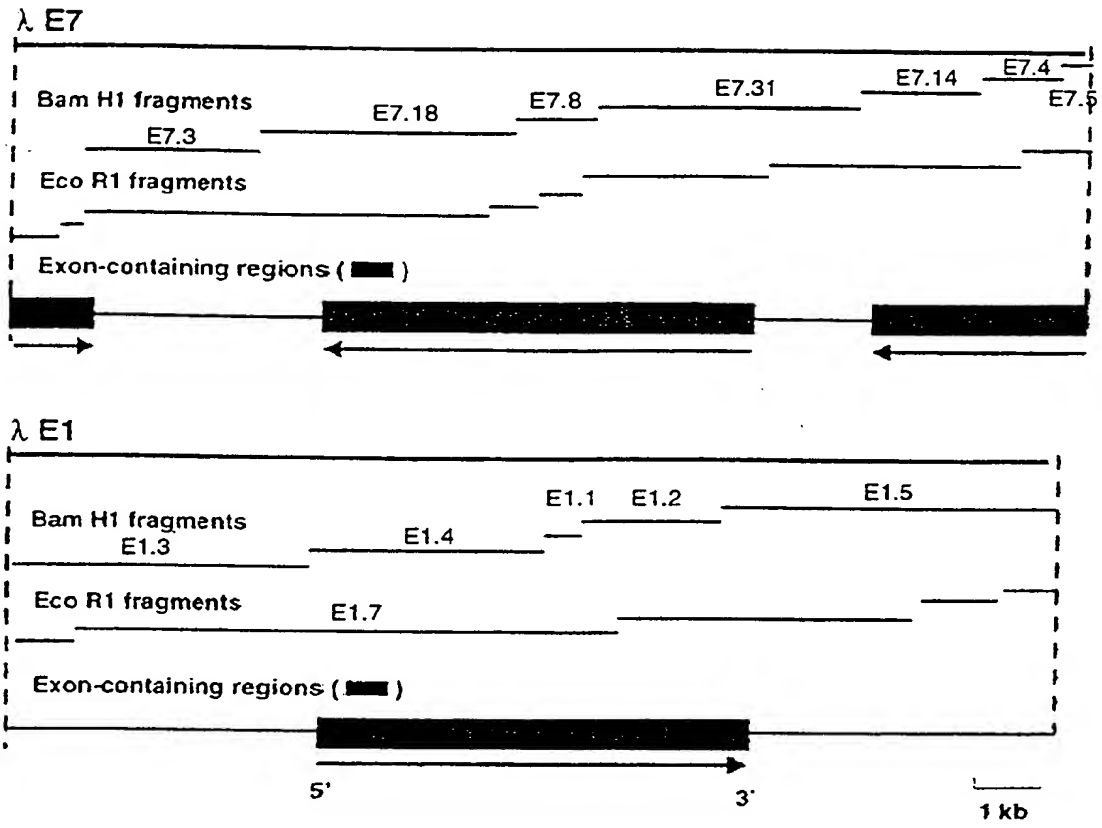

λ E7
Bam H1 fragments
E7.3
E7.18
E7.8
E7.31
E7.14
E7.4
E7.5
Eco R1 fragments
Exon-containing regions ( )
λ E1
Bam H1 fragments
E1.3
E1.4
E1.1
E1.2
E1.5
Eco R1 fragments
E1.7
Exon-containing regions ( )
5'
3'
1 kb

FIGURE 3

```
                1                                                   50
RSBEI           .......... .********* *....***pl lp******** **ag******
MSBEI           .......... .*****v*p** **tplp***r ***h***aa* pg********
D4cDNA          .......... .*****ap*c **sl..***p **pa****g* **s*......
PESBEII         .......... .......... .......... .......... ..........
POSBE           meinfkvlsk pirgsfp*f* pkv*sgas*n kic*psqh*t *lkf*sqers
D2cDNA          .......... .****s**ll prp*a*.... ....****l* *******ggk
Consensus       ---------- -MLCLTSSSS SP-S-APPR- SRS-ADRPSP GIIAGGGNVR

                51                                                  100
RSBEI           l..**v*... *p*****g** *tn***pa** rk****v*vv ***..*****
MSBEI           l..**l**qc ka***gv*** ****ataa*v q*d*****ak g**..*****
D4cDNA          .......... .......... ******p*s* prdy****a* *g*..gd***
PESBEII         .......... .......... ........mt d*ks**psv* **f..*nig*
POSBE           w..d*s*t*k *rv*kde*mk h*saisa*lt d**s***pl* ***kt*nigl
D2cDNA          rlsv*p***f ll**l****a ***sf*s*** rg**ia**.. tgygs*****
Consensus       ---SV-SVP- S-RRSWPRKV KSKFSV-VTA -DNKTMAT-E EDV--DHLPI

                101                                                 150
RSBEI           ********e* ****n**i** *****c**** ********** *********v
MSBEI           ********i* ********** *****gs**e n**s**s*** *********n
D4cDNA          *******ag* ****s****k ******s*** ********** **********
PESBEII         lnv*ss**p* ****k***** **h**k***e y****q**a* ******f*r*
POSBE           ln***t**p* l****h**** *v***m**** y**p****aq ******f*r*
D2cDNA          ****l**ae* ****d*trn* *i******** ***s****** **********
Consensus       YDLDPKLE-F KDHFRYRMKR YLDQKHLIEK HEGGLEEFSK GYLKFGINTE

                151                                                 200
RSBEI           *g******** ********** *******ak* *****k**** **k*******
MSBEI           *dg******* ******e*** ***d***a** *****k**** **k*d**k**
D4cDNA          nd******** ***m****** ********g* r*t**n**** **********
PESBEII         *dgis***** *******i** ***g*****l h****q**** **q*pdad*n
POSBE           *gci****** *****dev** ***g****** m****q**** ****pd*ds*
D2cDNA          hg*s****** ***e****** ********g* **a**n**** **********
Consensus       --ATVYREWA PAAQEAQLIG DFNNWNGSNH KMEKD-FGVW SIRISHVNGK

                201                                                 250
RSBEI           ********** ***r**g*a* ********** **f******* **********
MSBEI           ********** ***l*.g*** ******l*** ********** **********
D4cDNA          ********** ***hr*d*l* ********** **f******* **********
PESBEII         ********r** ***k*sd*** ********k* ****ptr*a* *****y****
POSBE           *v******r** ***k**n*** ********k* **a**t**a* *****y****
D2cDNA          ********** ***r*.h*** **q******* ***t**es** ****l*****
Consensus       PAIPHNSKVK FRF-HG-GVW VDRIPAWIRY ATVDASKFGA PYDGVHWDPP

                251                                                 300
RSBEI           ac******** ********** ********** ********** **********
MSBEI           a****t**** **s**a**** ********** k*a******* **********
D4cDNA          sg******** **r******* ********** r********* ********k*
PESBEII         l****q**** *****k**** ********ss **r*ns**** **d******e
POSBE           p****h**y* *****r**** ********ss **r*ns**** **d*****k*
D2cDNA          s******n** ******v*** ******v**g kl*ag***** p*****cl**
Consensus       -SERYVFKHP RPPKPDAPRI YEAHVGMSGE EPEVSTYREF ADNVLPRIRA
```

Figure 4

```
                301                                                    350
RSBEI           ********** ********** ******.*** ********** **********
MSBEI           ********** ********** ******.*** ********** **********
D4cDNA          ********** *****ilcf* w******.*** ********** **********
PESBEII         ********** ********** w*****kp*** ******s*** **********
POSBE           ********** *******g** ******.*** ****y*n*** **********
D2cDNA          t********g *****ds*** ******.*** ********** **********
Consensus       NNYNTVQLMA IMEHSYYASF GYHVTN-FFA VSSRSGTPED LKYL-DKAHS

                351                                                    400
RSBEI           ********** ********** *********n *h******t** **********
MSBEI           ********** ********** ********** *******a** **********
D4cDNA          ********** *****s*m** *********n *******t** **********
PESBEII         ***n****** ********** ********** s*q*****a** **********
POSBE           ***q**v*** ********** *********g s*******a** **********
D2cDNA          ********** ********i* ********** ah*****yt** k**n***ng*
Consensus       LGLRVLMDVV HSHASNNVTD GLNGYDVGQS TQESYFH-GD RGYHKLWDSR

                401                                                    450
RSBEI           ********** ********** ********** ********** *****k*****
MSBEI           ********** ********** ********** ********** *****v*****
D4cDNA          ********** ********** ********** *********n ******s*a*
PESBEII         *******ks. s********** ****k***** ********** ******a****
POSBE           ********** ********** ****n***** *********v **********
D2cDNA          ********** ********** ********** *v*******n *n****s*n*
Consensus       LFNYANWEVL RFLLSNLRYW -DEFMFDGFR FDGVTSMLYH HHGINMGFTG

                451                                                    500
RSBEI           ********** ********** *******l** ********** **********
MSBEI           **q******* a********** *******l** ********** **********
D4cDNA          ******g*** ********** *******i** ********** ********s**
PESBEII         d*n****e** ********** **s*v*di** ***d****** ***g*g***s
POSBE           **n****ea* ********** **n*i**i** ********** ***g*g***s
D2cDNA          *****ig*** n***f***** *******l** **i***v*** **********
Consensus       NYKEYFSLDT DVDAVVYMML ANHLMHK-LP EATVVAEDVS GMPVLCRPVD

                501                                                    550
RSBEI           ********** ********** *******rk* ****.*vq** **********
MSBEI           ********** ********** ********** **g*.*ah** **********
D4cDNA          ********** ********** *******l** ***a.*ah** **********
PESBEII         *v********* ******k*** *****k**** **k*.*sln* **********
POSBE           ********** ******k*** *****n*e** **k*.*tss* **********
D2cDNA          ***l*****q **t******** **e**g*qq* ***sv*sq** *****p**f*
Consensus       EGGVGFDYRL AMAIPDRWID YLKNKDDSEW SMSE-I--TL TNRRYTEKCI

                551                                                    600
RSBEI           ********** ********** ******t*** *********n **********
MSBEI           ********** ********** ******t*** ********** **********
D4cDNA          ********** *****m**** ******t*** ********** **********
PESBEII         s********* ********** **e***ss** c*tml***** ***s*h****
POSBE           ********** ********** ******s*** c*td***v** *****h****
D2cDNA          ****rqnh** **s**m**** **w*t*s*** a*d*d***** *a*********
Consensus       AYAESHDQSI VGDKTIAFLL MDKEMY-GMS DLQPASPTID RGIALQKMIH
```

Figure 4 (cont..)

```
                601                                                  650
RSBEI       ********** ********** ********** ********** .*********
MSBEI       ********** ********** ********** ********** .*********
D4cDNA      ********** ********** ********** ********** .*****s*i*
PESBEII     ********** ********** ********** **g******* lt**n****n
POSBE       *f******** ********** ********** ********** .***n*a*s*
D2cDNA      *********s **k*****.. .......... .......... ..........
Consensus   FITMALGGDG YLNFMGNEFG HPEWIDFPRE GNNWSYDKCR -RQWSLVDTD

                651                                                  700
RSBEI       ********** *********e ********** ******k*** **********
MSBEI       ********** *********r ********** ********** **********
D4cDNA      ********** ********** ********** *******k** **********
PESBEII     ********** *r***l**** **i*a*t*** **st*n**** **********
POSBE       ********** *r***s**** ****a*g*** **s*d**n** **********
D2cDNA      .....***** v**vdtps** c******n*t a*h******g sa*tk*....
Consensus   HLRYKYMNAF DQAMNALD-K FSFLSSSKQI VSDMNEE-KV IVFERGDLVF

                701                                                  750
RSBEI       ******n*** k********* ********** **v******* **********
MSBEI       ******k*** ********** ********** **v******* **********
D4cDNA      ******s*** ********** ***k****** **m******* aqyn******
PESBEII     ******en** ********** ********** *te******* ***a*q****
POSBE       ******kn** ********** ********** *we******t **********
D2cDNA      .*thlrsgc* *p.....s** stssc**... .*gpsnqspf skpfig*pgc
Consensus   VFNFHP-KTY EGYKVGCDLP GKYRVALDSD AL-FGGHGRV GHDVDHFTSP

                751                                                  800
RSBEI       **m******* *****..... .......... .....***** **********
MSBEI       ********** *****..... .......... .....***** **********
D4cDNA      ********** *****..... .......... .....***** **********
PESBEII     ********** *****..... .......... .....***** ****h***v*
POSBE       ********** **g*qipskc cllrehvwli telmnacq*l kitrq*f*vs
D2cDNA      ifcc*lfkge *......... .......... .......... ..........
Consensus   EG-PGVPETN FNNRP----- ---------- -----NSFKV LSPPRTCVAY

                801                                                  850
RSBEI       *...****dr **l*rg**va s**i.vte** **e**s.... ..**ti**gw
MSBEI       *...****ag agr*lhak*e t***s**es* **k*s*.... ..a....ssk
D4cDNA      *...****ka *kpkde**** w**aa*g.** **e***vkda ad**at**sk
PESBEII     *...*****q **snnpnlg* *ee**a*adt **aripdvs* e*..ed*nld
POSBE       *yqqp*sr*v trnlkirylq *sv**tna*q klkf**qtf* v*yyqqpilr
D2cDNA      .......... .......... .......... .......... ..........
Consensus   Y---RVDER- EE-R--GAAS -GKT-PA-YI DV-ATR---- -SGE--SG--

                851                  876
RSBEI       kg***d*cg* **mk***r** *e*c*d
MSBEI       edk*atagg* **wk*arqp* *q*t**
D4cDNA      ka*tgg*ss* **in***g*p *k*n*.
PESBEII     r*e*ns**av dagi*kvere vvgdn*
POSBE       r*tr*lk*sl stnist*... ......
D2cDNA      .......... .......... ......
Consensus   --SEK-DD-K KG--FVF-SS D-D-K-
```

Figure 4 (cont..)

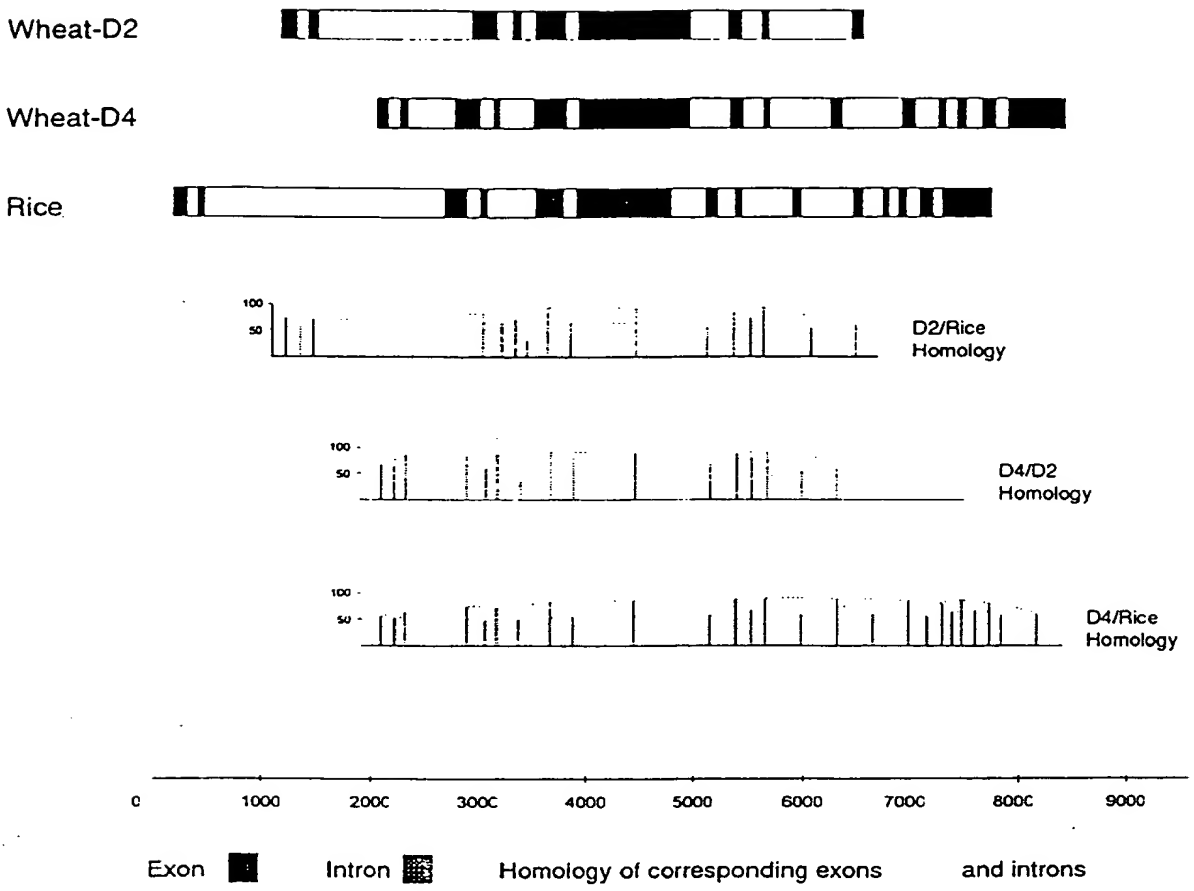

Wheat-D2
Wheat-D4
Rice
100
50
D2/Rice Homology
100
50
D4/D2 Homology
100
50
D4/Rice Homology
0
1000
2000
3000
4000
5000
6000
7000
8000
9000
Exon
Intron
Homology of corresponding exons and introns

FIGURE 5

DNA
5' TCCCGTGTCTGCGCCAAGAGACTACACCATGGCAACAGCTGAAGATGGTGTTGGCGACCT 5'
3' AGGGCACAGACGCGGTTCTCTGATGTGGTACCGTTGTCGACTTCTACCACAACCGCTGGA 3'
possible reading frames
S R V C A K R L H H G N S * R W C W R P
P V S A P R D Y T M A T A E D G V G D L
P C L R Q E T T P W Q Q L K M V L A T F
true N-terminal sequence for BE-1 (Morell et al, 1997)
V S A P R D Y T M A T A E D G V

Figure 6

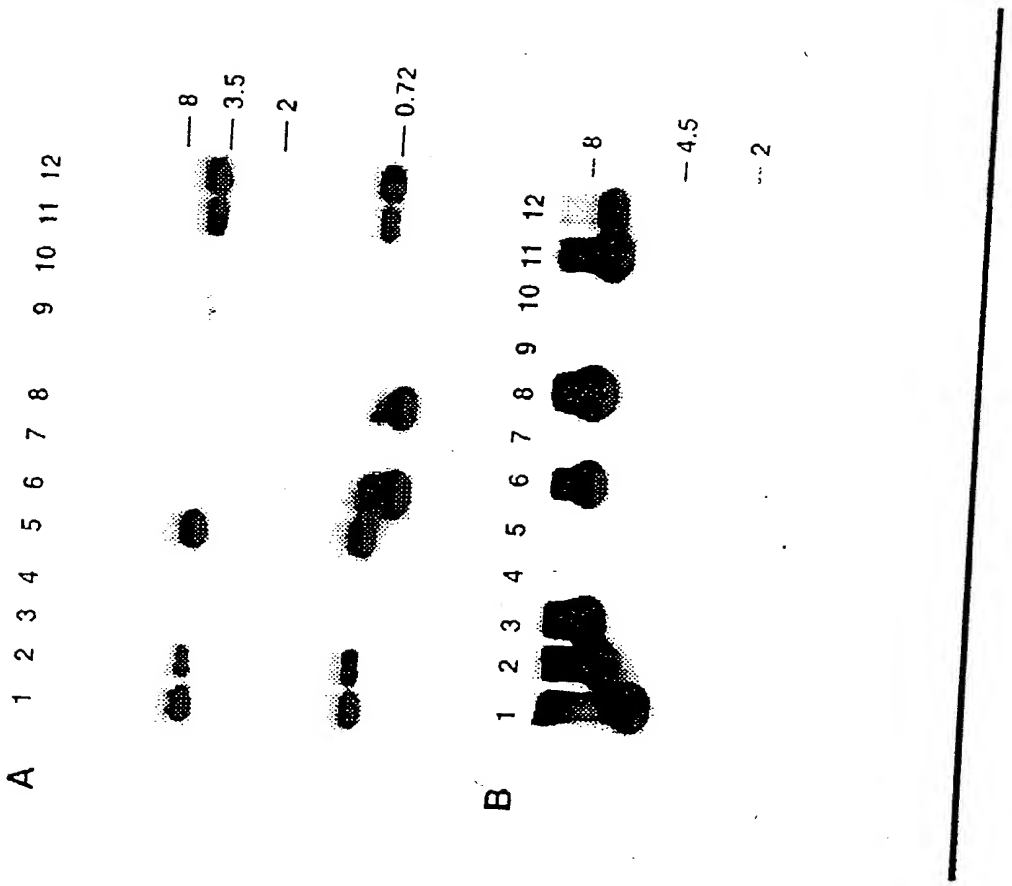


FIGURE 7

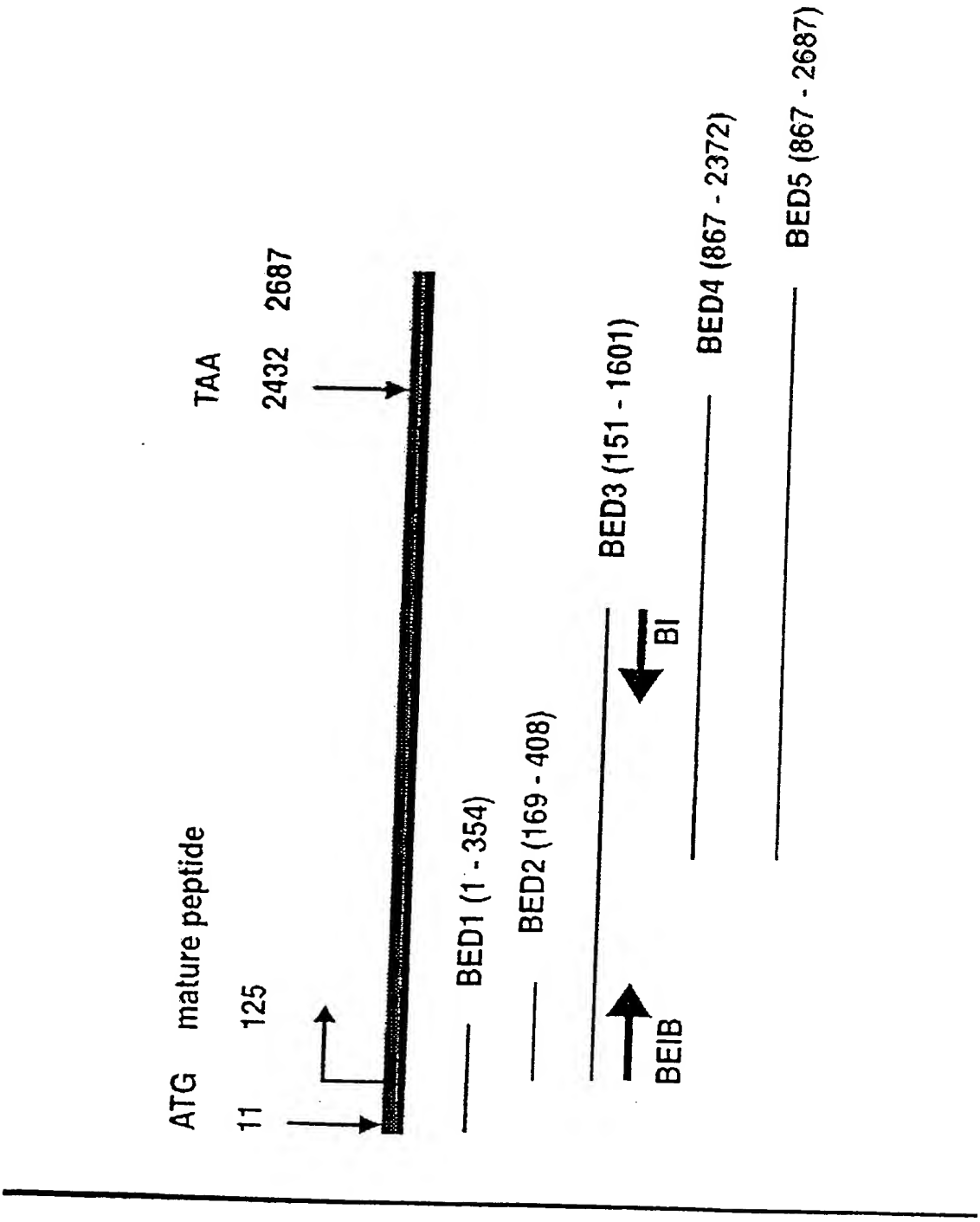

ATG
11
mature peptide
125
TAA
2432
2687
BED1 (1 - 354)
BED2 (169 - 408)
BED3 (151 - 1601)
BI
BEIB
BED4 (867 - 2372)
BED5 (867 - 2687)

FIGURE 8

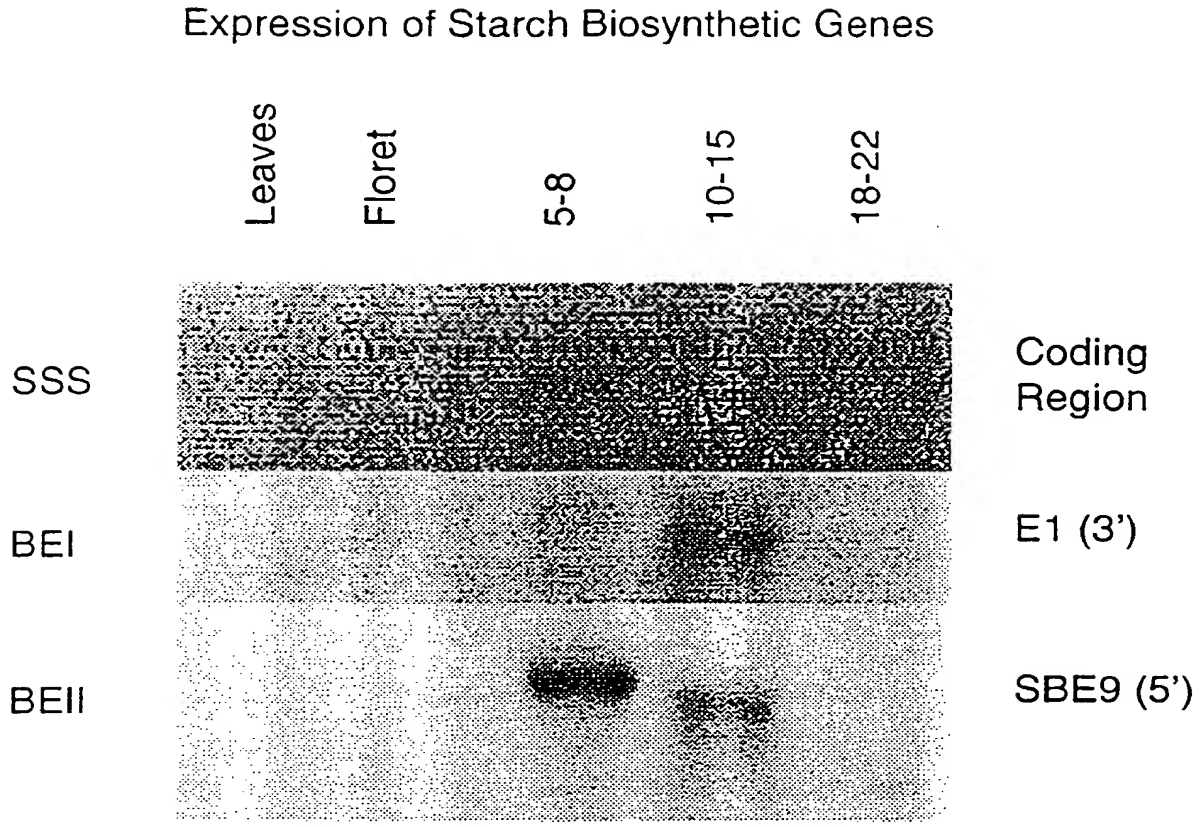

Expression of Starch Biosynthetic Genes
Leaves
Floret
5-8
10-15
18-22
SSS
BEI
BEII
Coding Region
E1 (3')
SBE9 (5')

FIGURE 9A

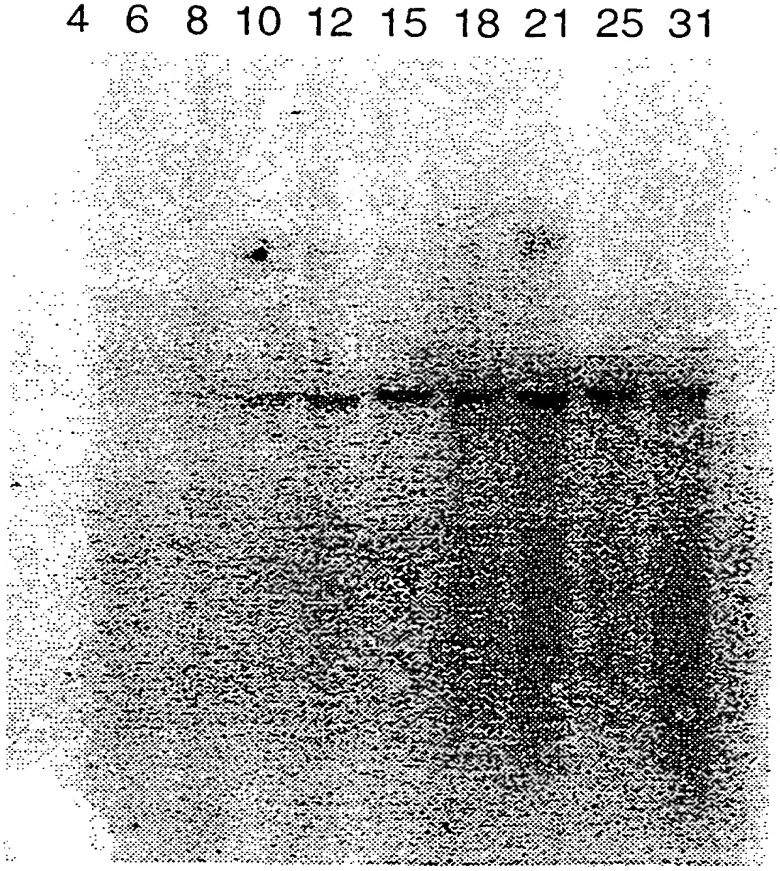


FIGURE 9B

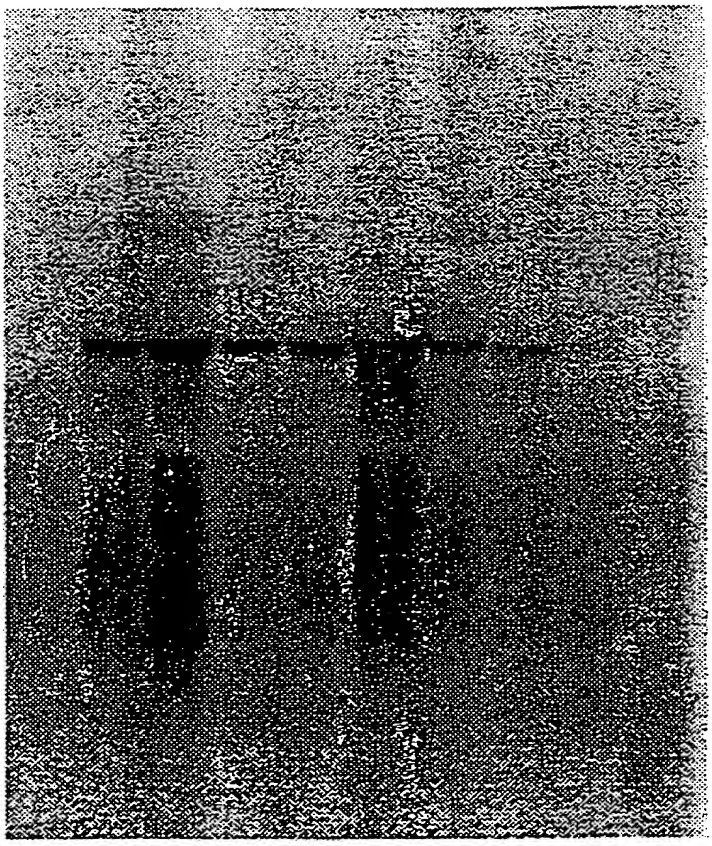


FIGURE 9C

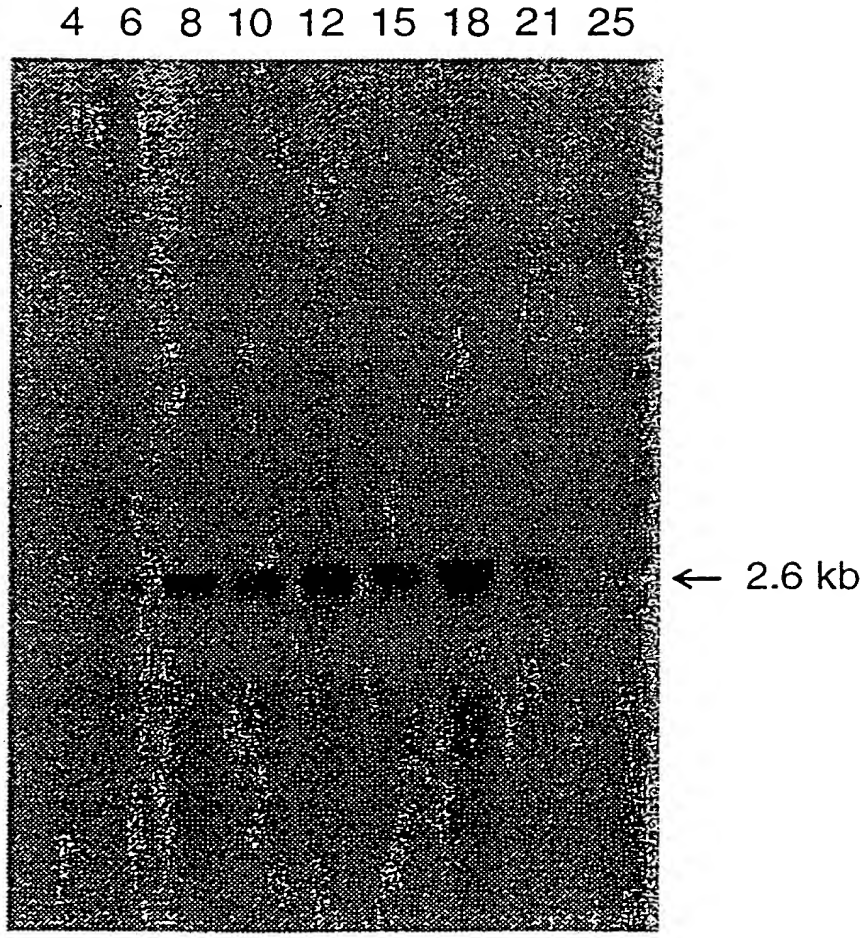


FIGURE 9D

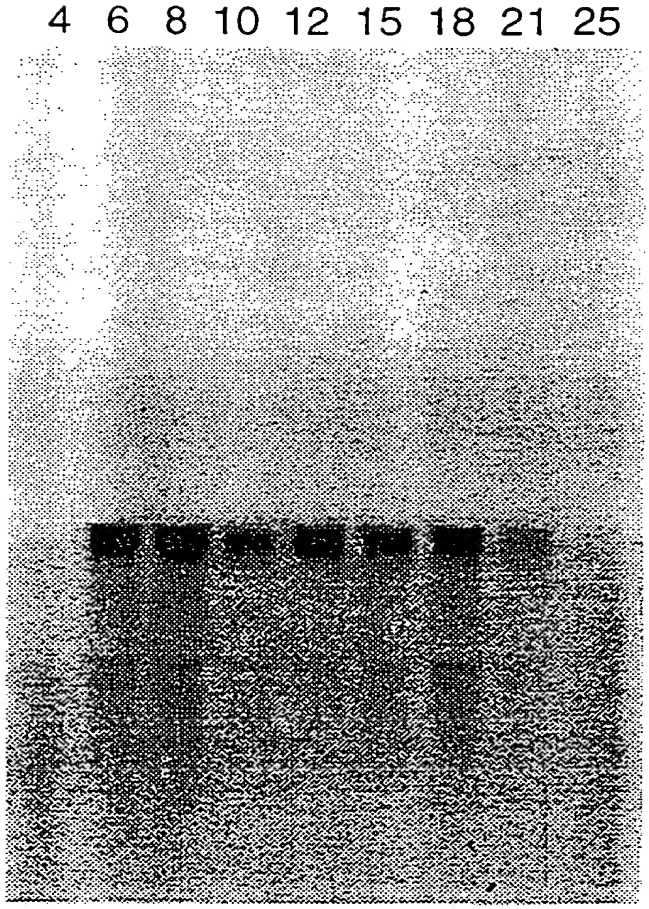


FIGURE 9E

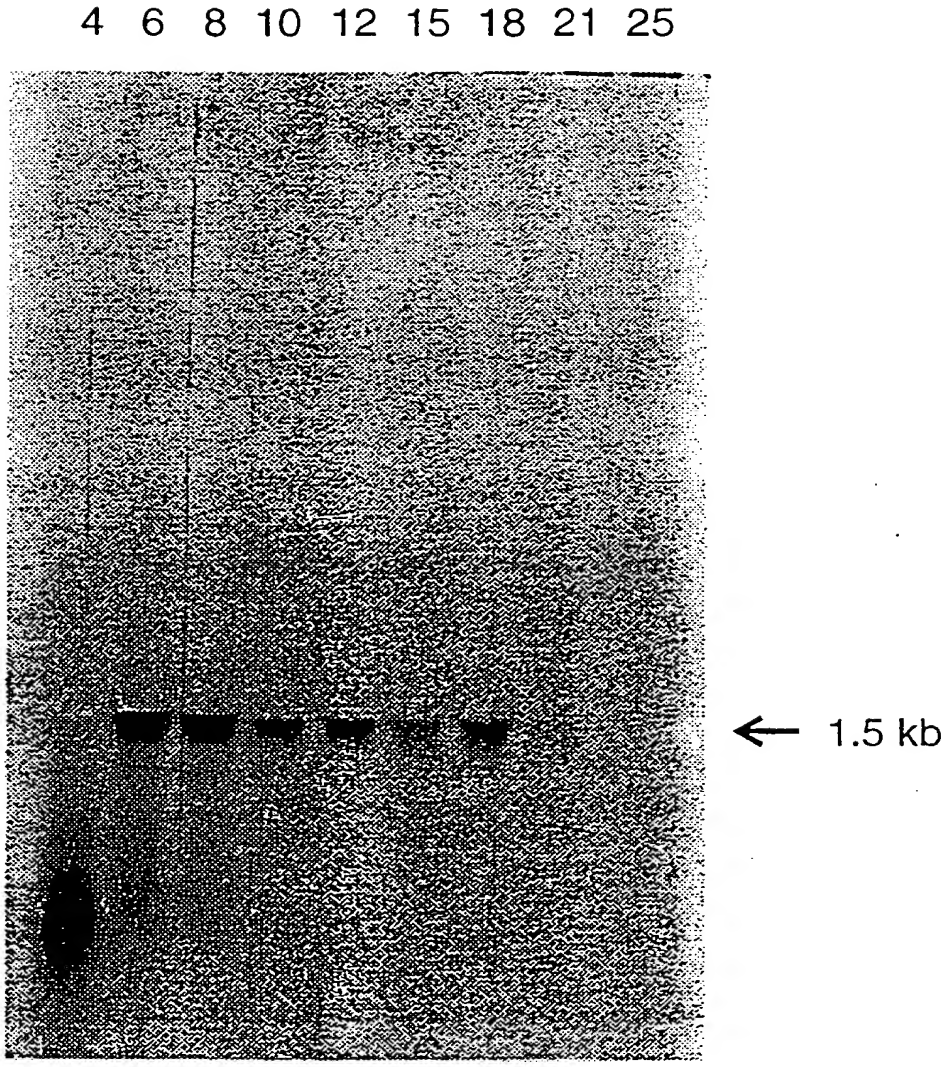


FIGURE 9F

4 6 8 10 12 15 18 21 25

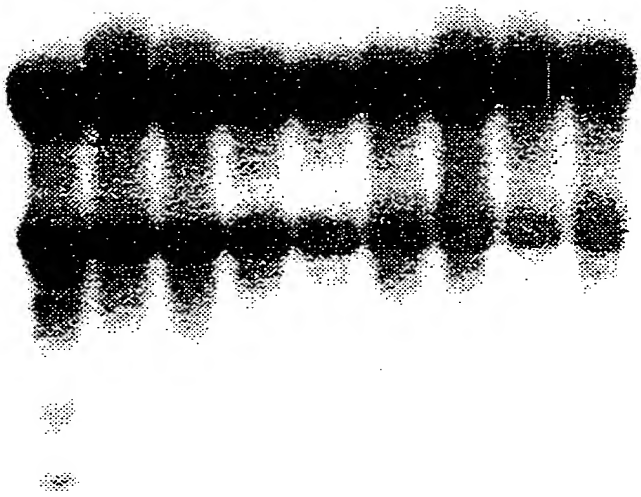


FIGURE 9G

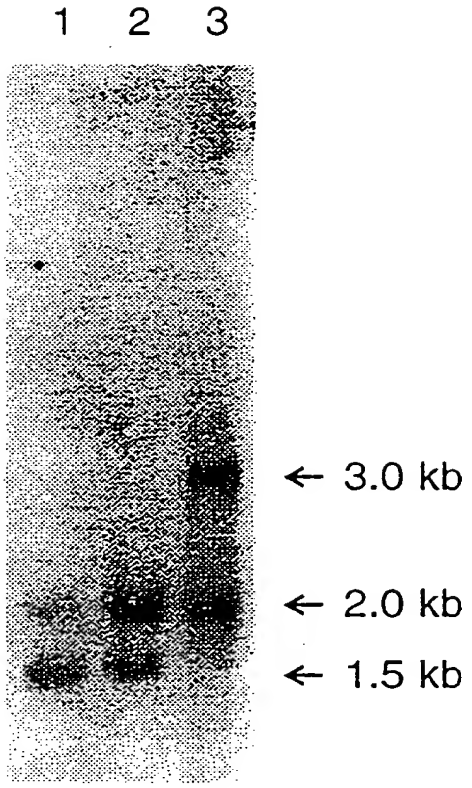


FIGURE 9H

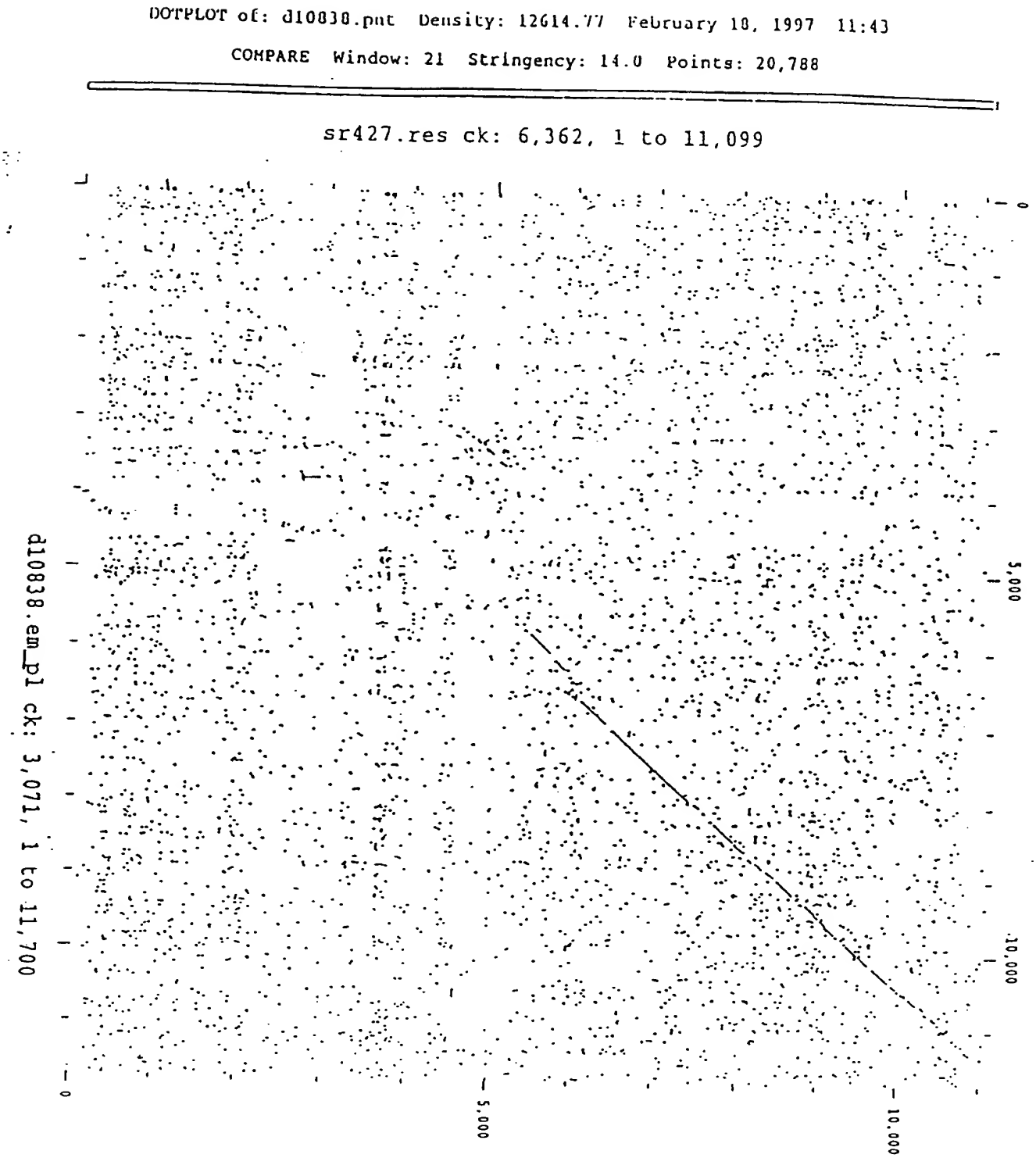

DOTPLOT of: d10838.pnt Density: 12614.77 February 18, 1997 11:43
COMPARE Window: 21 Stringency: 14.0 Points: 20,788
sr427.res ck: 6,362, 1 to 11,099
d10838.em_pl ck: 3,071, 1 to 11,700
0
5,000
10,000
0
5,000
10,000

Figure 10

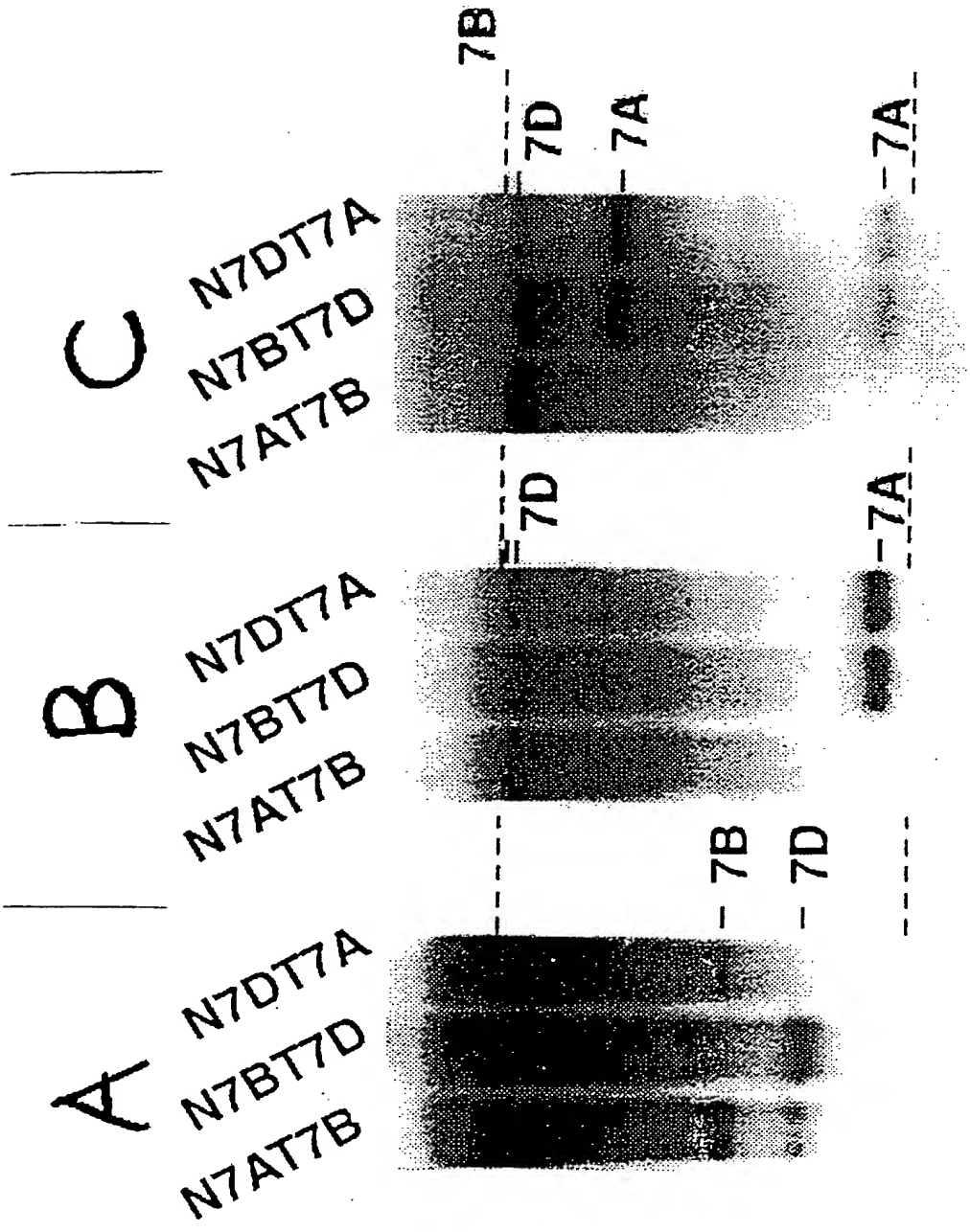

7B
7D
7A
7A
C
N7DT7A
N7BT7D
N7AT7B
7D
7A
B
N7DT7A
N7BT7D
N7AT7B
7B
7D
A
N7DT7A
N7BT7D
N7AT7B

FIGURE 11

Genomic Clones from *T.tauschii*
for SBE II.

BamH I EcoRI

FIGURE 12

N-terminal sequences of cereal starch branching enzymes

Protein	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
	A																					
RICEBEI[B]	A	T	A	R	K	N	K	T	M	V	T	V	V	E	E	V						
WBE-I_{AD}	V	S	A	P	R	D	Y	T	M	A	T	A	E	D	G	V						
MAIZE BEI[C]	A	T	V	Q	E	D	K	T	M	A	T	A	K	G	D	V						
RICEBEII[D]	A	A	G	A	S	G	E	-	V	M	I	P	E	G	E	S	D	G	M	P	V	S
WBE-II		A	A	S	P	G	K	-	V	L	V	P	D	G	E	S	D	D	L	A	S	Y
MAIZE BEII[E]	A	A	A	A	A	R	K	A	V	M	V	P	E	G	E	N	D	G	L	A	S	

[A] N-terminal amino acid of the mature polypeptide. [D] Kawasaki *et al.*(1993), [C] Baba *et al.* (1991),

[D] Mizuno *et al.* (1993),[B] Fisher *et al.* (1993)

Residues in the wheat sequences showing identity with the respective maize or rice branching enzyme isoforms are highlighted in bold text.

Figure 13a

PCT/AU98/00743
09/508377

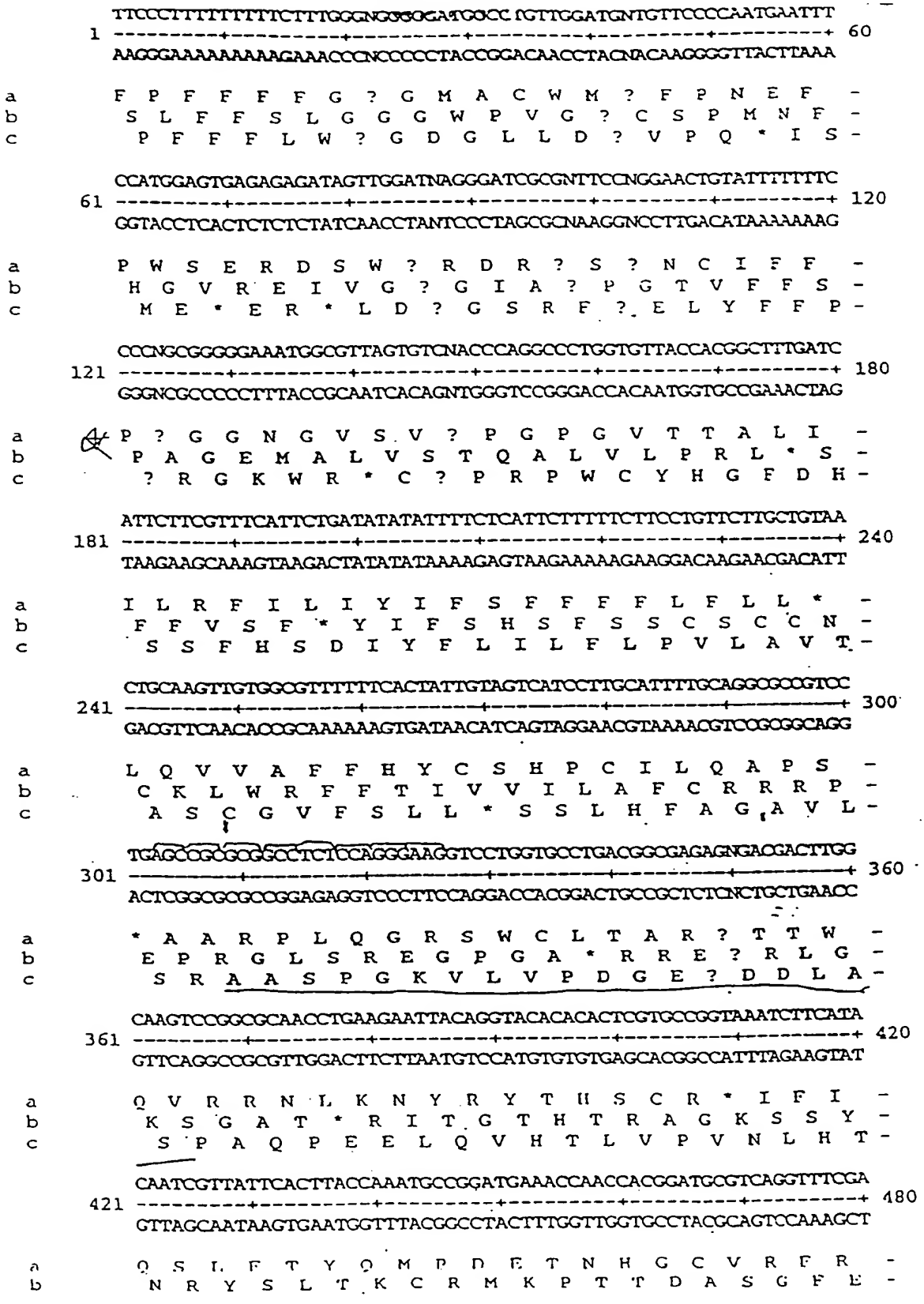
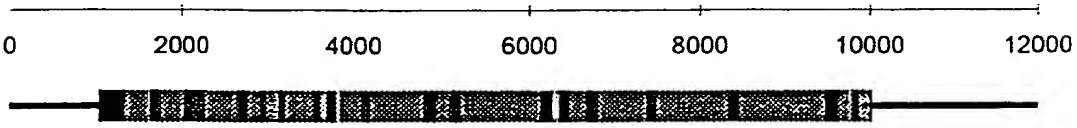


Figure 13b

Branching Enzyme-II Genes

Intron/Exon structure of wheat BE-II



Schematic Diagram of a cDNA for BE-II

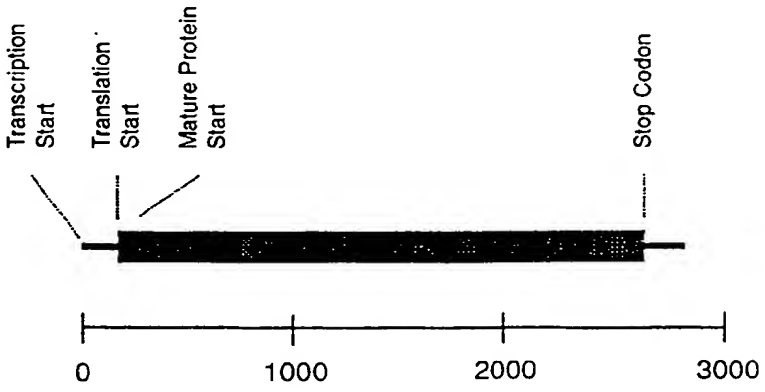


FIGURE 14

Wheat DNA probed with the
5' conserved sequence of SBE II.

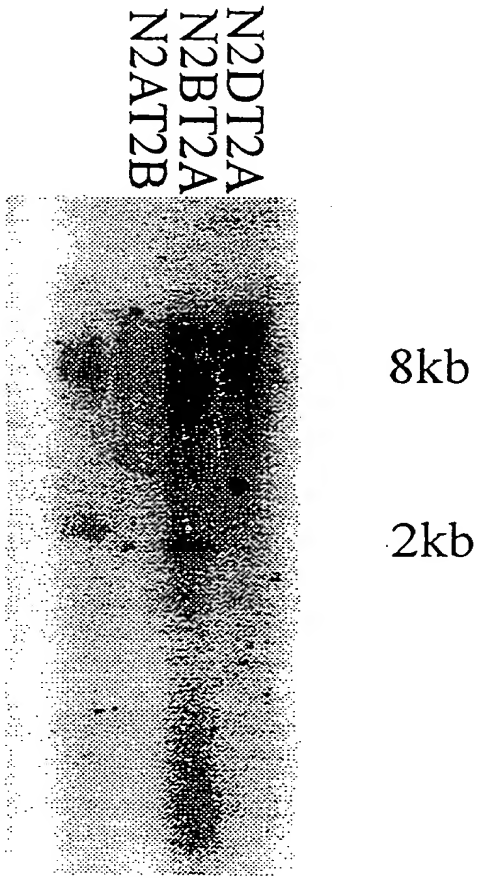


FIGURE 15

COMPARISON OF N-TERMINAL SEQUENCES
OF SOLUBLE STARCH SYNTHASE

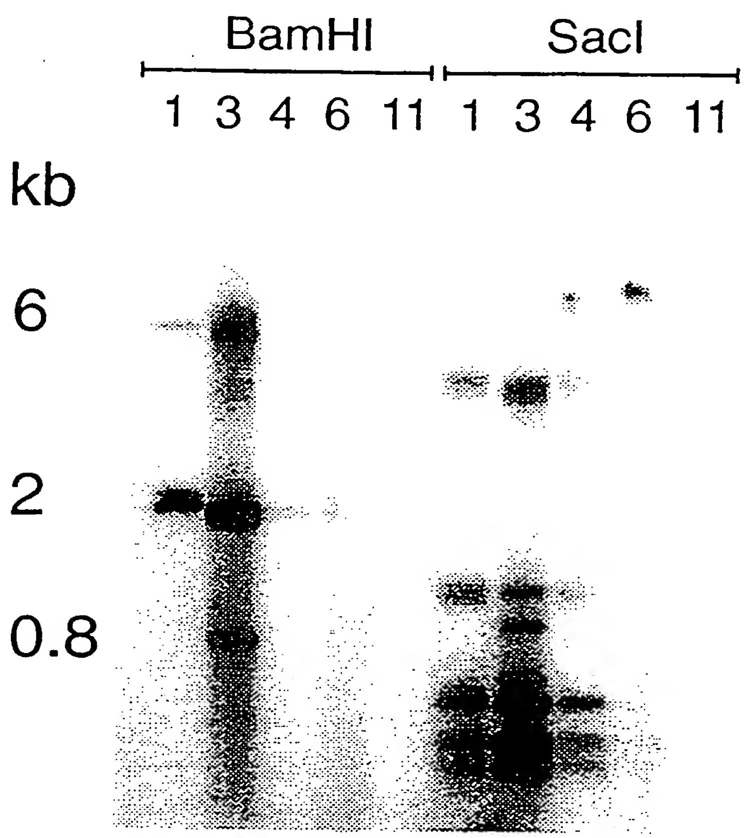
GRYVAELSREGPAARP Deduced from wheat cDNA

GPYVAELSPEGPAAPP Wheat N-terminal

Figure 16

09/508377

Soluble Starch Synthase Genomic Clones



Probed with SM-2 full length cDNA

FIGURE 17

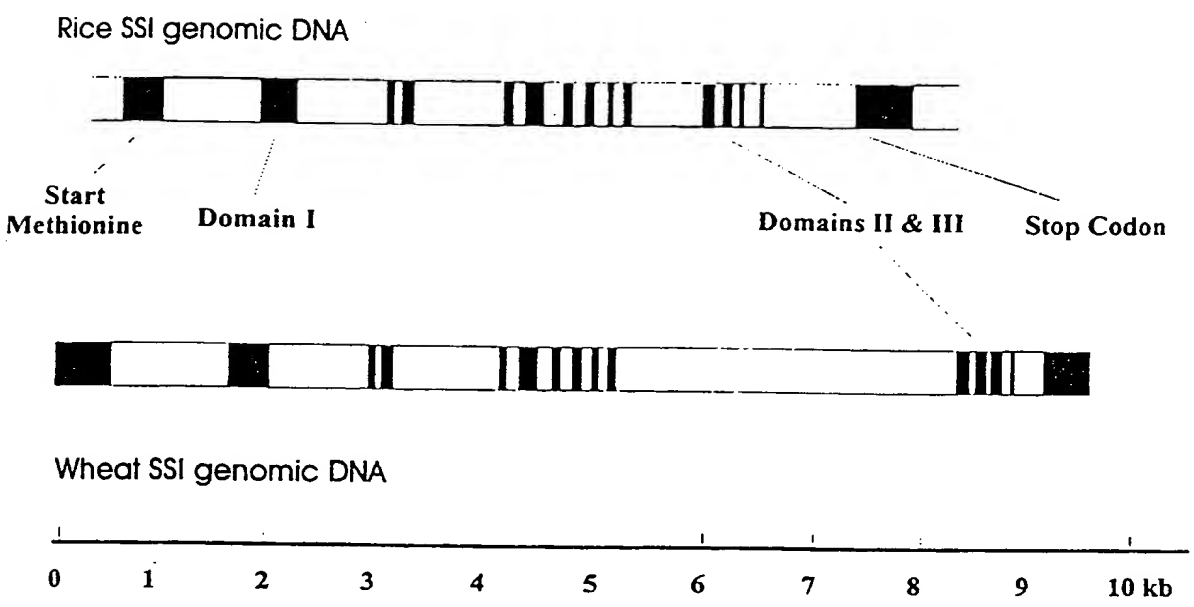

INTRON EXON STRUCTURE - Wheat SSI
Rice SSI genomic DNA
Start Methionine
Domain I
Domains II & III
Stop Codon
Wheat SSI genomic DNA
0
1
2
3
4
5
6
7
8
9
10 kb

FIGURE 18

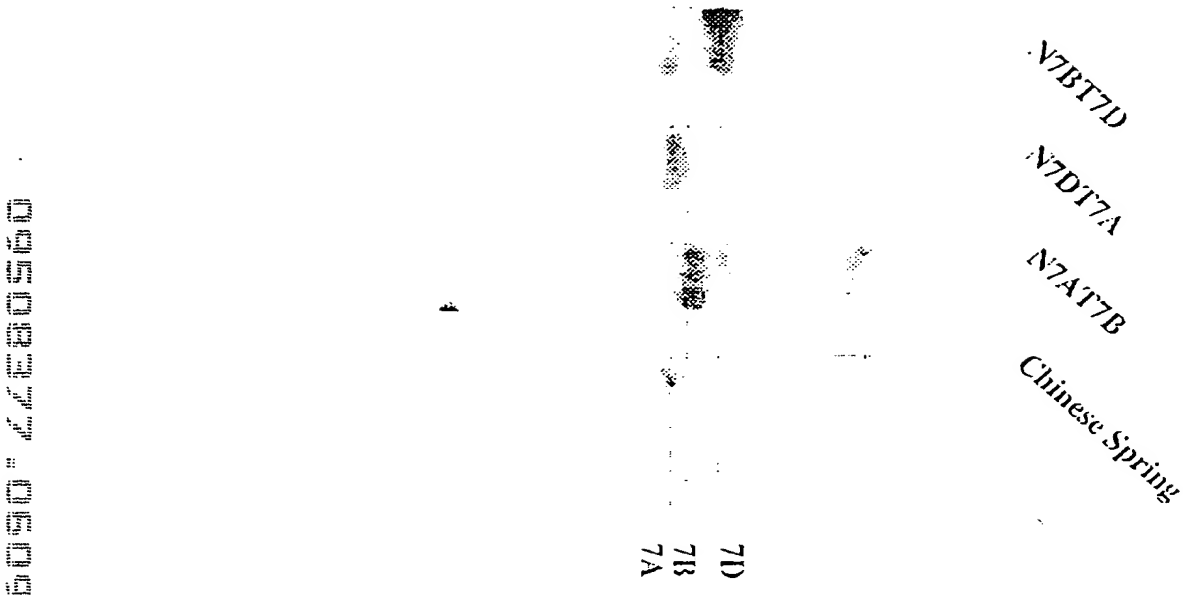


FIGURE 19

```
                ATACTACATACTATATGCTTGCACCCAAGGGACACTTTATAACTATTCTGGCTGTGGGA
             80 +----------+----------+----------+----------+----------+---- 139
                TATGATGTATGATATACGAACGTGGGTTCCCTGTGAAAATATTGATAAGACCGACACCCT

a                 T  T  Y  Y  Y  M  L  A  P  K  G  H  F  Y  N  Y  S  G  C  G  N  -
b              I  L  H  T  I  C  L  H  P  R  D  T  F  I  T  I  L  A  V  G  -
c              Y  Y  I  L  Y  A  C  T  Q  G  T  L  L  *  L  F  W  L  W  E  -

                ATACCTTCAACTGTAATCATCCTGTGGTTCGTCAATTCATTGTAGATTGTTTAAGATACT
            140 +----------+----------+----------+----------+----------+---- 199
                TATGGAAGTTGACATTAGTAGGACACCAAGCAGTTAAGTAACATCTAACAAATTCTATGA

a                 T  F  N  C  N  H  P  V  V  R  Q  F  I  V  D  C  L  R  Y  W  -
b              I  P  S  T  V  I  I  L  W  F  V  N  S  L  *  I  V  *  D  T  -
c              Y  L  Q  L  *  S  S  C  G  S  S  I  H  C  R  L  F  K  I  L  -

                GGGTGACGGAAATGCATGTTGATGGTTTTCGTTTGACCTT
            200 +----------+----------+----------+----------+----------+ 240
                CCCACTGCCTTTACGTACAACTACCAAAAGCAAAACTGGAA

a                 V  T  E  M  H  V  D  G  F  R  F  D  L  -
b              G  *  R  K  C  M  L  M  V  F  V  L  T  -
c              G  D  G  N  A  C  *  W  F  S  F  *  P  -

Enzymes that do cut:

    NONE

Enzymes that do not cut:

    EcoRI
```

Figure 20a

Comparison of Wheat Debranching Enzyme-I (WDBE-I) PCR fragment with maize *Sugary*-1 DNA sequence

```
                1098      1107      1117      1127      1137      1147      1157
SUGARY.DNA      TGAGGTGATCATGGATGTTGTCTTCAATCATACAGCTGAAGGTAATGAGAAAGGCCCAAT
                ||||||||||||||||||||||||||| |||||||||||| ||||||||||| || ||||||
WHEAT1.DNA      ....GTGATCATGGATGTTGTCTTCAACCATACAGCTGAGGGTAATGAGAATGGTCCAAT
                   -3        6        16        26        36        46        56

                1158      1167      1177      1187      1197      1207      1217
FILE NAME       ATTATCCTTTAGGGGGATAGATAATAGTACATACTACATGCTTGCACCTAAGGGAGAGTT
SUGARY.DNA      |||||| |||||||||| | ||||||| |||||||||| |||||||||||| |.|.||
WHEAT1.DNA      ATTATCATTTAGGGGGTCGATAATACTACATACTATATGCTTGCACCCAAGGGACACTT
                   57        66        76        86        96       106       116

                1218      1227      1237      1247      1257      1267      1277
FILE NAME       TTATAATTATTCTGGTTGTGGAAATACCTTCAATTGTAATCATCCTGTAGTCCGTGAATT
SUGARY.DNA      |||||| |||||||||| ||||| |||||||||| |||||||||||||| || ||| ||||
WHEAT1.DNA      TTATAACTATTCTGGCTGTGGGNATACCTTCAACTGTAATCATCCTGTGGTTCGTCAATT
                   117       126       136       146       156       166       176

                1278      1287      1297      1307      1317      1327      1337
FILE NAME       TATAGTGGATTGCTTGAGATACTGGGTAACAGAAATGCATGTTGATGGTTTTCGTTTTGA
SUGARY.DNA      || || |||||  || || |||||||| || |||||||||||| |||||||||||||||||
WHEAT1.DNA      CATTGTAGATTGTTTAAGNTACTGGGTGACGGAAATGCATGTTGNTGGTTTTCGTTTTGA
                   177       186       196       206       216       226       236

                1338      1347      1357
FILE NAME       CCTTGCATCTATACT-G...
SUGARY.DNA      ||||||||||  ||
WHEAT1.DNA      CCTTGCATCTN--CTTNAAA
                   237       246       256

MATCHING PERCENTAGE
    TOTAL WINDOW          84%   ( 219/  260)
    ALIGNMENT WINDOW      86%   ( 219/  253)
```

Figure 20b

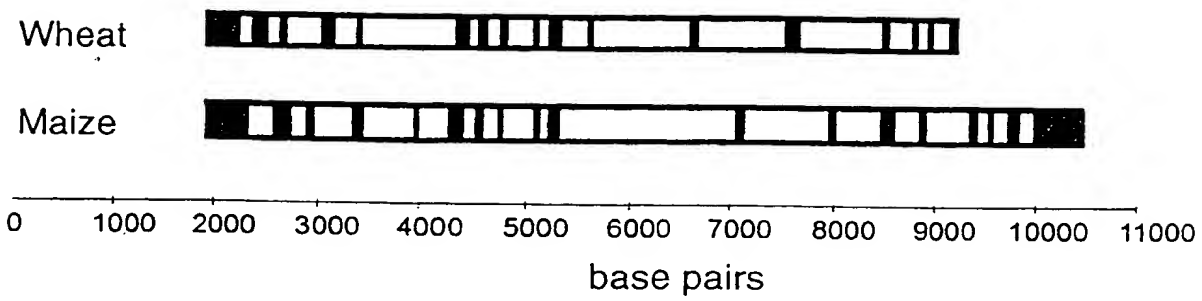
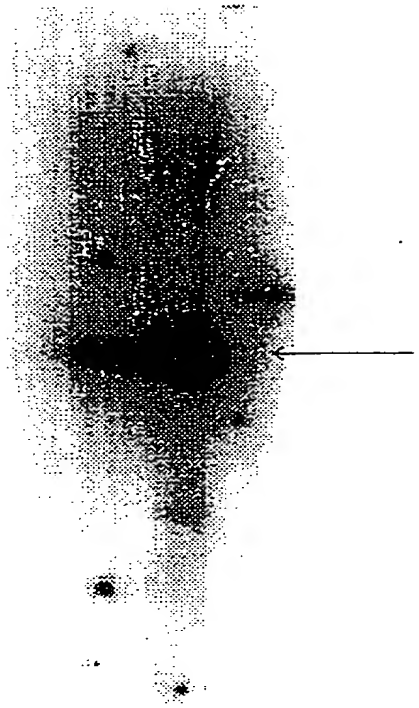

Wheat
Maize
0
1000
2000
3000
4000
5000
6000
7000
8000
9000
10000
11000
base pairs

FIGURE 20C

Southern blot of T. *tauschii* Genomic DNA

1X 3X



BamHI Digest

T. tauschii Genomic DNA Probed With The Wheat Debranching Enzyme PCR Product

FIGURE 21A

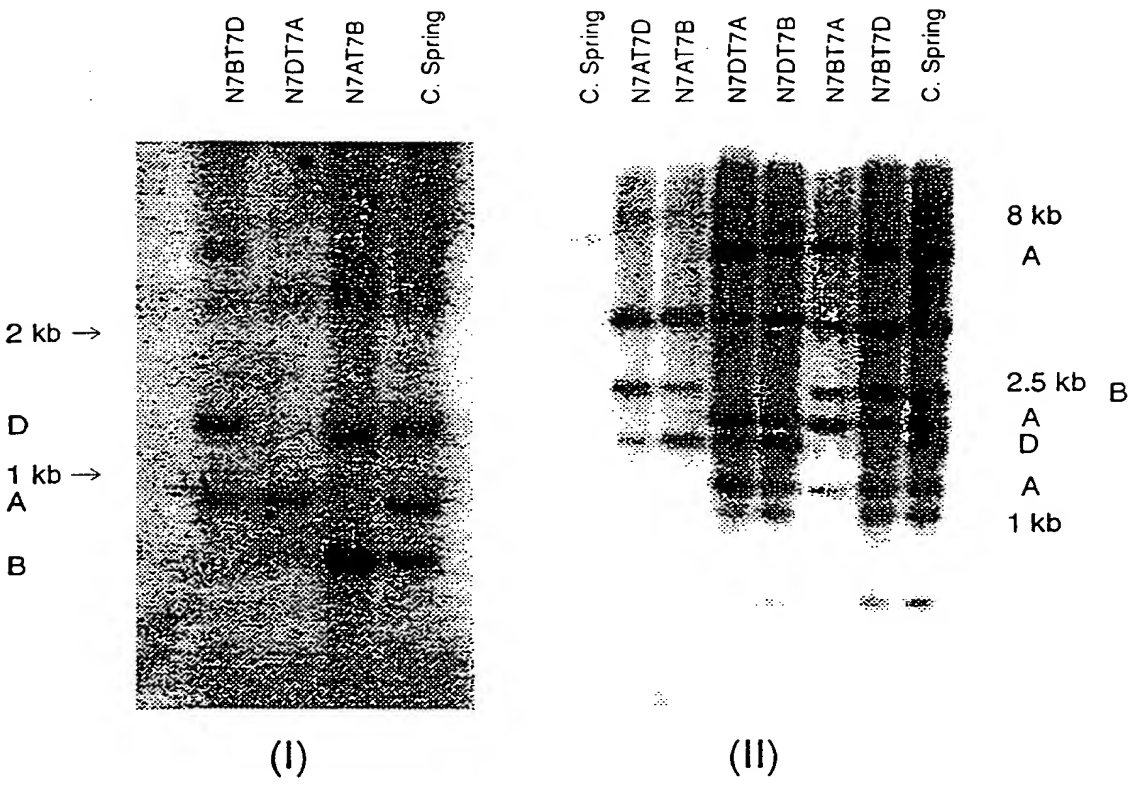

N7BT7D
N7DT7A
N7AT7B
C. Spring
2 kb →
D
1 kb →
A
B
(I)
C. Spring
N7AT7D
N7AT7B
N7DT7A
N7DT7B
N7BT7A
N7BT7D
C. Spring
8 kb
A
2.5 kb
B
A
D
A
1 kb
(II)

FIGURE 21B

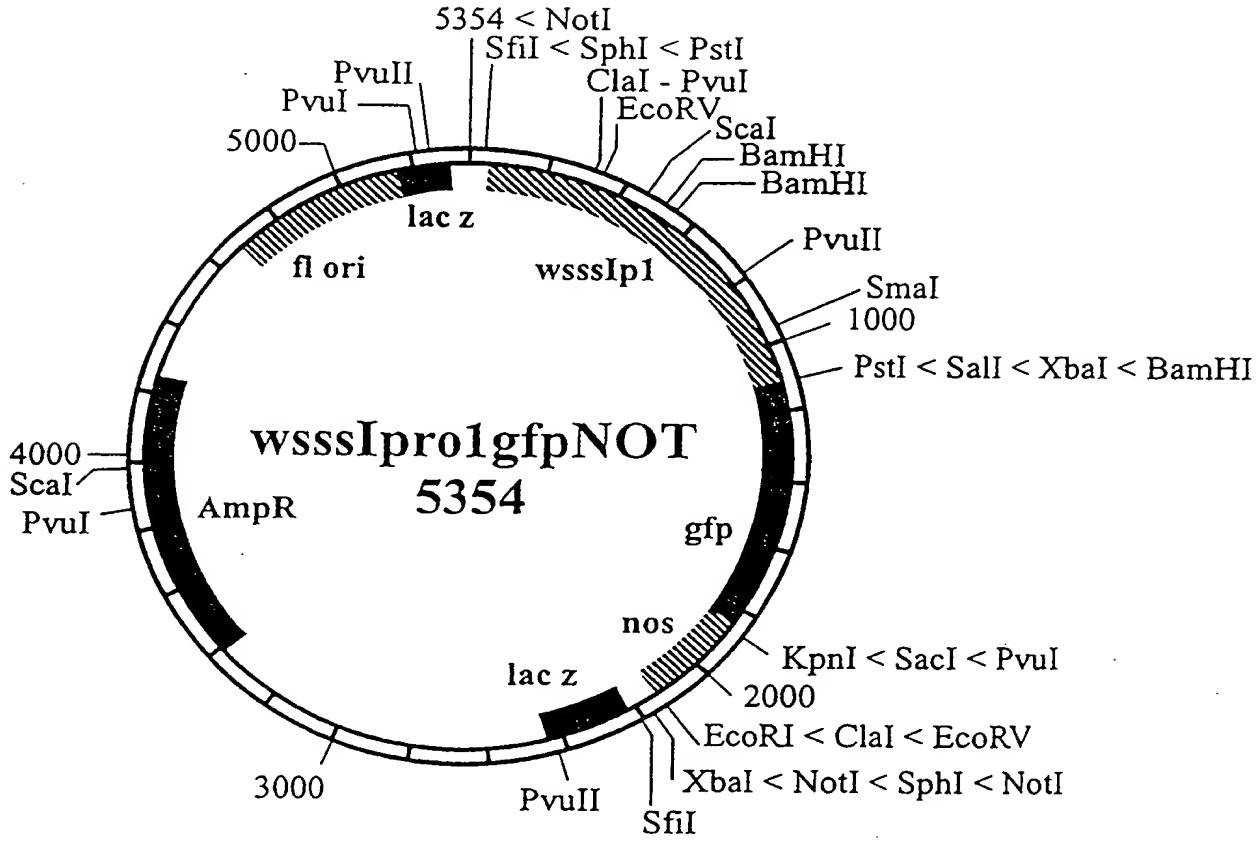

5354 < NotI
SfiI < SphI < PstI
ClaI - PvuI
EcoRV
ScaI
BamHI
BamHI
PvuII
SmaI
1000
PstI < SalI < XbaI < BamHI
PvuII
PvuI
5000
lac z
fl ori
wsssIp1
wsssIpro1gfpNOT
5354
4000
ScaI
PvuI
AmpR
gfp
nos
KpnI < SacI < PvuI
2000
lac z
EcoRI < ClaI < EcoRV
XbaI < NotI < SphI < NotI
3000
PvuII
SfiI

FIGURE 22A

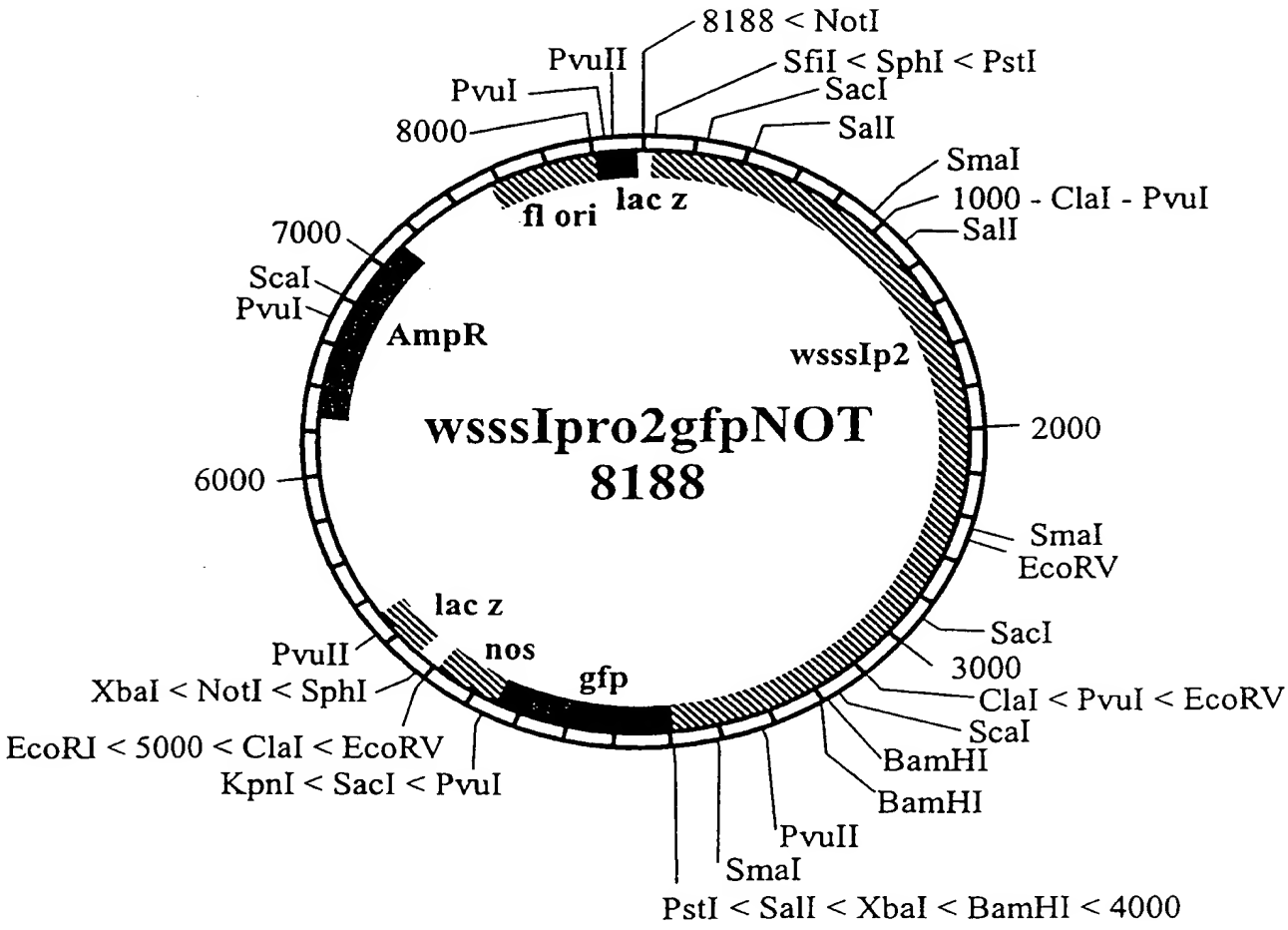

8188 < NotI
PvuII
SfiI < SphI < PstI
PvuI
SacI
8000
SalI
SmaI
lac z
1000 - ClaI - PvuI
fl ori
SalI
7000
ScaI
PvuI
AmpR
wsssIp2
wsssIpro2gfpNOT
8188
2000
6000
SmaI
EcoRV
lac z
SacI
PvuII
nos
3000
XbaI < NotI < SphI
gfp
ClaI < PvuI < EcoRV
ScaI
EcoRI < 5000 < ClaI < EcoRV
BamHI
KpnI < SacI < PvuI
BamHI
PvuII
SmaI
PstI < SalI < XbaI < BamHI < 4000

FIGURE 22B

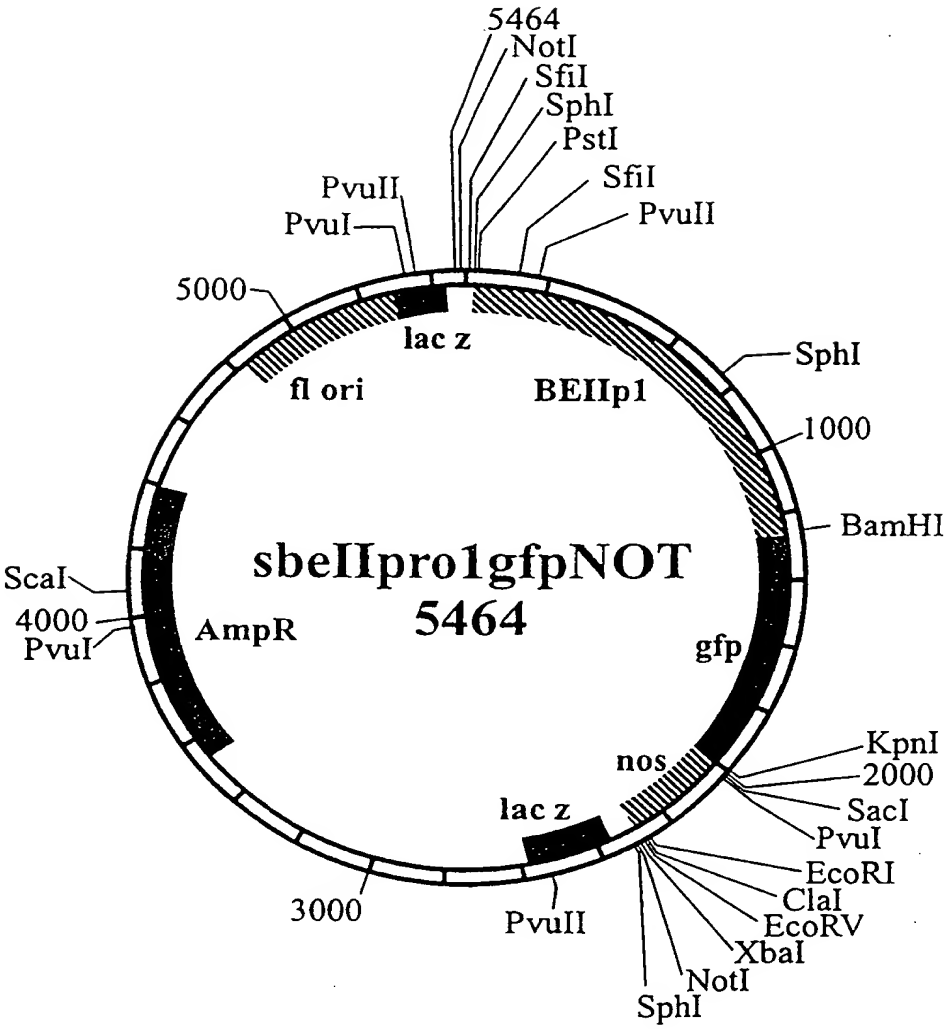

5464
NotI
SfiI
SphI
PstI
SfiI
PvuII
PvuII
PvuI
5000
lac z
SphI
fl ori
BEIIp1
1000
BamHI
sbeIIpro1gfpNOT
5464
ScaI
4000
PvuI
AmpR
gfp
KpnI
nos
2000
SacI
lac z
PvuI
EcoRI
ClaI
EcoRV
XbaI
NotI
SphI
3000
PvuII

FIGURE 22C

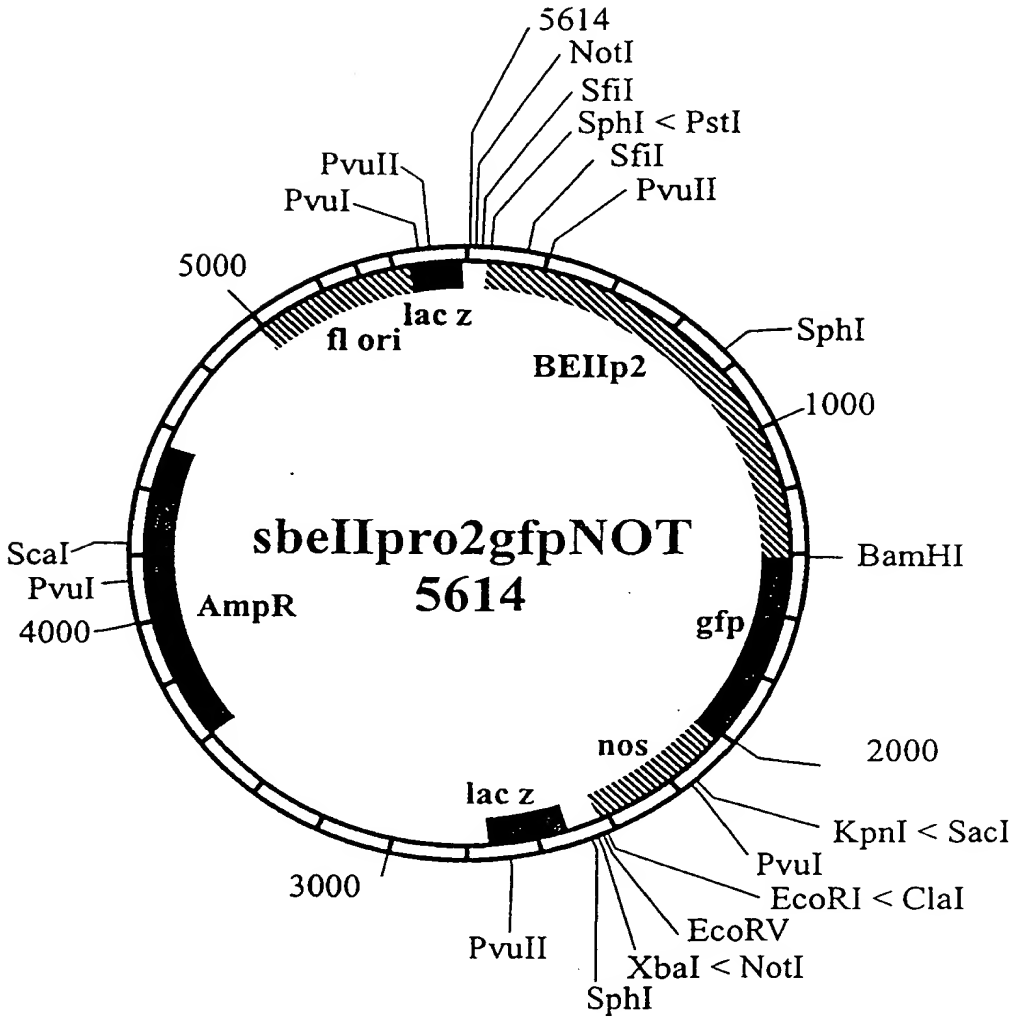

5614
NotI
SfiI
SphI < PstI
SfiI
PvuII
PvuII
PvuI
5000
lac z
fl ori
BEIIp2
SphI
1000
sbeIIpro2gfpNOT
5614
ScaI
PvuI
4000
AmpR
BamHI
gfp
nos
2000
lac z
KpnI < SacI
PvuI
EcoRI < ClaI
EcoRV
XbaI < NotI
SphI
PvuII
3000

FIGURE 22D

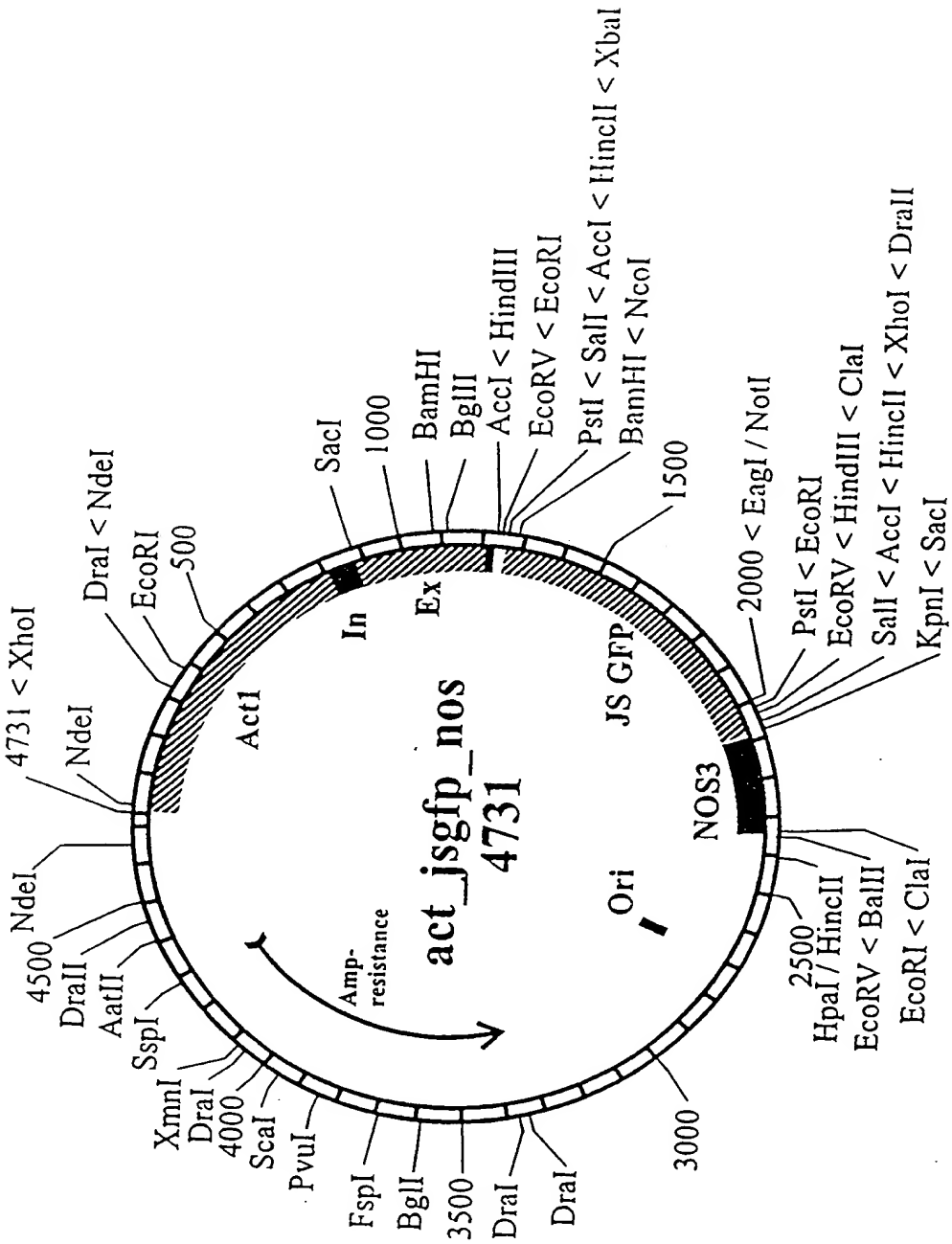
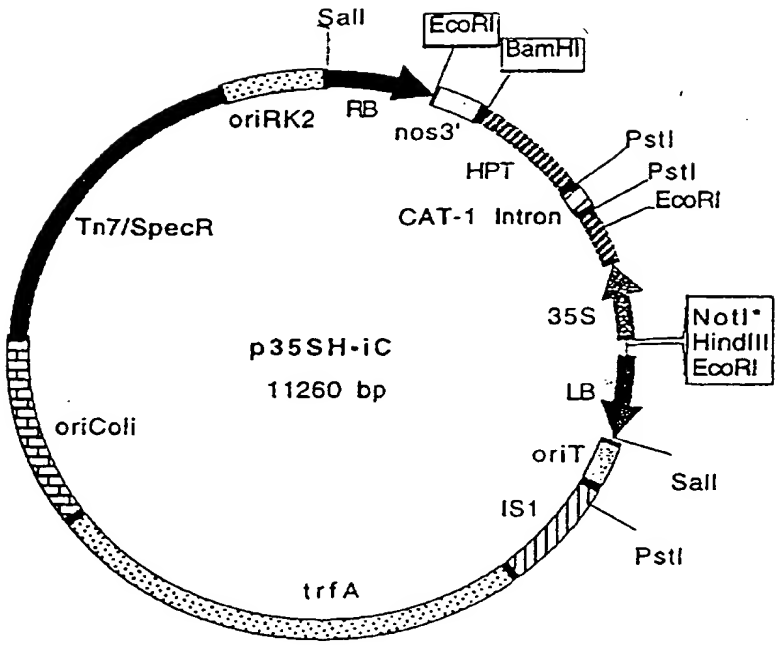

act_jsgfp_nos
4731
Act1
In
Ex
JS GFP
NOS3
Ori
Amp-resistance
4731 < XhoI
NdeI
DraI < NdeI
EcoRI
500
SacI
1000
BamHI
BglII
AccI < HindIII
EcoRV < EcoRI
PstI < SalI < AccI < HincII < XbaI
BamHI < NcoI
1500
2000 < EagI / NotI
PstI < EcoRI
EcoRV < HindIII < ClaI
SalI < AccI < HincII < XhoI < DraII
KpnI < SacI
EcoRI < ClaI
2500
HpaI / HincII
EcoRV < BalII
3000
DraI
DraI
3500
BglII
FspI
PvuI
ScaI
4000
DraI
XmnI
SspI
AatII
DraII
4500
NdeI

Figure 22E


SalI
EcoRI
BamHI
RB
oriRK2
nos3'
PstI
HPT
PstI
EcoRI
CAT-1 Intron
Tn7/SpecR
35S
NotI*
HindIII
EcoRI
p35SH-iC
11260 bp
LB
oriColi
oriT
SalI
IS1
PstI
trfA

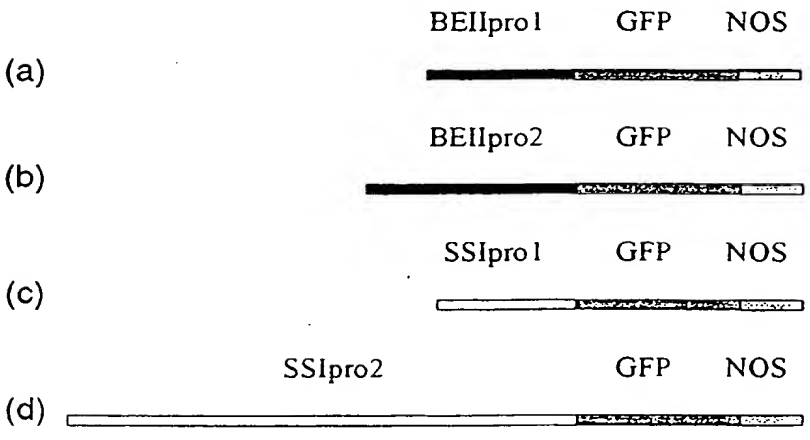

BEIIpro1 GFP NOS
(a)
BEIIpro2 GFP NOS
(b)
SSIpro1 GFP NOS
(c)
SSIpro2 GFP NOS
(d)

FIGURE 23

Primer Set	Key	Forward Primer	Forward Primer Sequence
1	E01'/E02	WBE2E1F	CGT CGC TGC TCC TCA GGA AG
2	E01/E02	sr854.1180F	CTG GCT GAC TCA ATC ACT ACG
3	E02/E03	WBE2E2F	CGC AAC CTG AAG AAT TAC AG
4	E03/E04	WBE2E3F	ATT TTC GGA GCC ATC TTG AC
5	E04/E05	WBE2E4F	TCG TGG TTA TGA AAA GCT TGG
6	E05/E06	sr913F	ATC ACT TAC CGA GAA TGG G
7	E05/I05	sr913F	ATC ACT TAC CGA GAA TGG G
8	E06/E07	WBE2E6F	ACA ATT GGA ATC CAA ATG CA
9	E07/E08	WBE2E7F	AGC TAT TCC TCA TGG CTC AC
10	E08/E09	WBE2E8F	TGC AGG CTC CAG GTG AAA TA
11	E10/E11	da5.seq	GGC TTG GAT ACA ATG CAG TGC
12	E12/E13	da151.seq	TTG ACG GCT TGA ATG GTT TC
13	E17/E18	WBE2E17F	TTT AGG TGG TGA AGG CTA TCT
14	E18/E19	sr860R	AAT GGA TAG ATT TTC CAA GAG G
15	E19_3'	WBE2-2395F	AGC AGA ACT GCG GTC GTG TA

Reverse Primer	Reverse Primer Sequence	Temp	bp
WBE2E2R	CAG GAC CTT CCC TGG AGA GG	57.4	401
WSBE9E2R	GGC ACG AGT GTG TGT ACC TGT A	57.7	601
sr866F	TAT CTT CAG GTA TCT ACA GC	49.8	309
WBE2E4R2	ATG CTT CCA ATC CAC CTT CA	-	>450
WBE2E5R	GAG CCC ATT CTC GGT AAG TGA	50.5	234
WBE2E6R	CTG CAT TTG GAT TCC AAT TG	49.9	232
WBE2I5R	CAG TAA GCT AGT TGG TGA ATA	46.6	106
WBE2E7R	GGG AGG AAA ATC TCC CAA AC	51.0	402
sr915F	CCA TTG AAA GGT ATT TCA CC	51.1	203
sr912F	TAA CTT ATT GAC ATA CCG G	48.4	439
WBE2E11R	CTG GAG TTC CAA AAC GGC TAC	51.2	289
WBE2E13R	ATT CTT CAA GCC ACC ATC TC	51.6	244
WBE2E18R	TAT TGT TAT TTC CAG GGG AGA	50.2	258
da23.seq	TGC TGC ATT GCC TGA TCG AA	50.4	~295
WBE2-2634R	AAC ACC CAG GCC CGT CCA TT	57.2	240

Figure 24

SBE II Intron 5 primer set - digested with Dde1

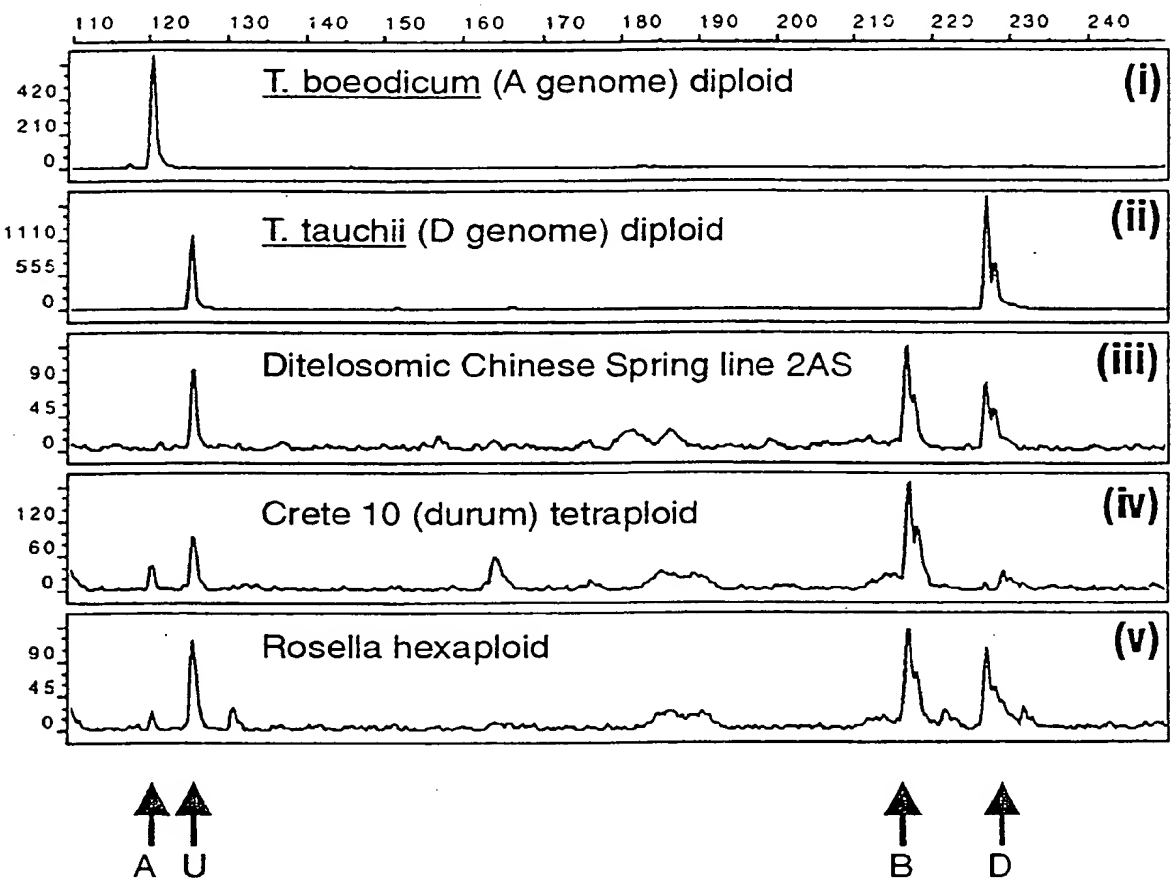


FIGURE 25

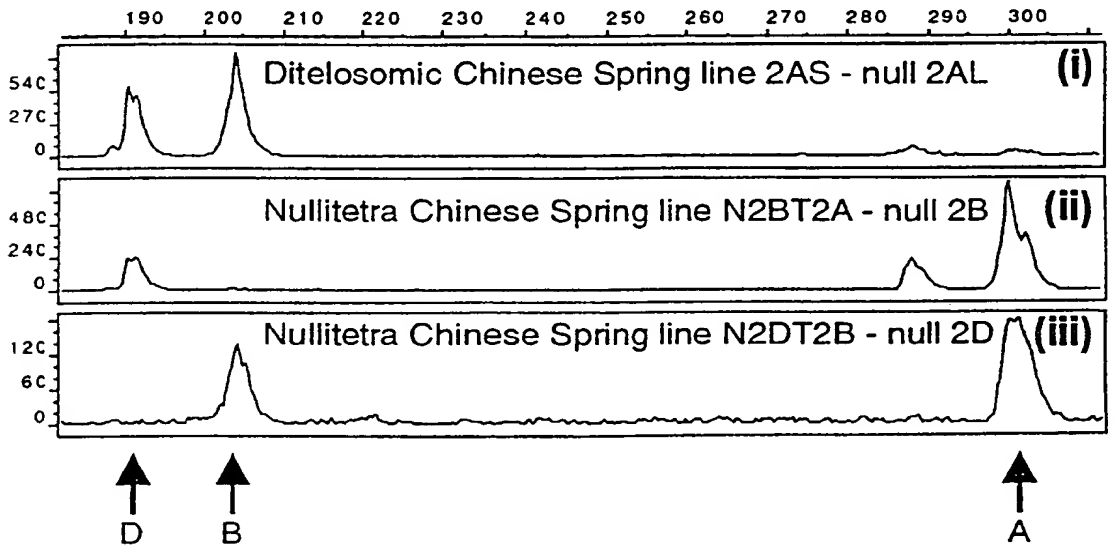

SBE II Intron 10 primer set - digested with Dde1
190
200
210
220
230
240
250
260
270
280
290
300
54C
27C
0
Ditelosomic Chinese Spring line 2AS - null 2AL
(i)
48C
24C
0
Nullitetra Chinese Spring line N2BT2A - null 2B
(ii)
12C
6C
0
Nullitetra Chinese Spring line N2DT2B - null 2D
(iii)
D
B
A

FIGURE 26

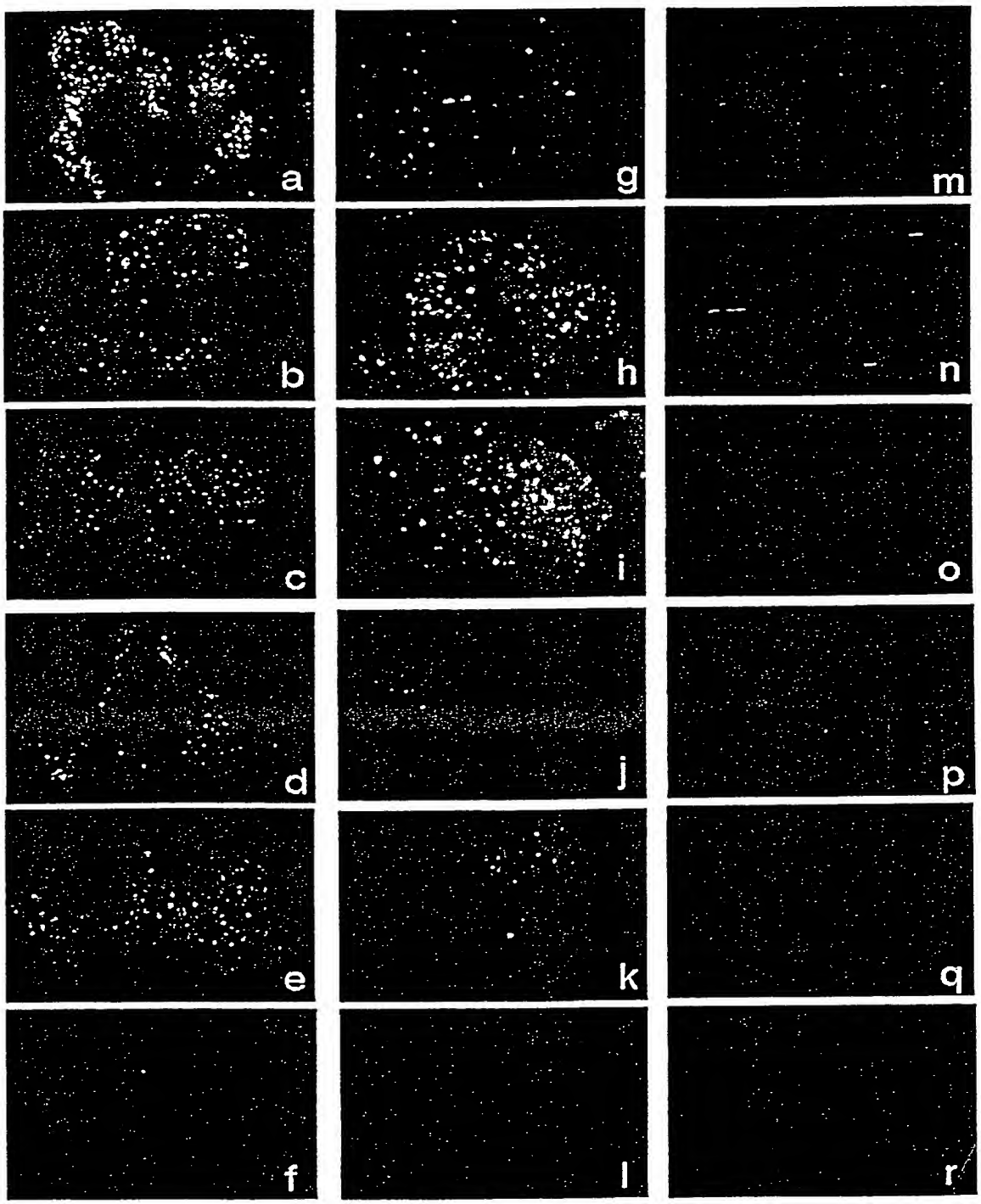


FIGURE 27